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OM nucleic - nucleic search, using sw model

Run on: September 6, 2005, 09:10:34 ; Search time 138 Seconds
(without alignments)
9141.807 Million cell updates/sec

Title: US-08-790-043B-1
Perfect score: 771
Sequence: 1 ATGTTAAATCTTGAAACAA.....GATTCACGCATTAATAA 771

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTOTUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	771	100.0	771	3	US-09-292-412-1
2	771	100.0	771	4	US-09-292-411A-1
3	506	65.6	916	4	US-10-138-701-5
4	437	56.7	704	4	US-08-956-171B-772
5	437	56.7	704	4	US-08-781-986A-772
6	63	8.2	587	4	US-08-956-171B-514
7	63	8.2	587	4	US-08-781-986A-514
8	30	3.9	39	4	US-10-089-740-1
9	30	3.9	39	4	US-09-292-411A-3
10	30	3.9	39	4	US-10-089-739-1
11	24	3.1	783	3	US-09-134-001C-1172
12	23	3.0	26	4	US-10-089-740-4
13	23	3.0	26	4	US-10-089-739-4
14	21	2.7	28	4	US-10-089-740-3
15	21	2.7	28	4	US-10-089-739-3
16	21	2.7	106929	4	US-09-949-016-12060
17	21	2.7	106929	4	US-09-949-016-16618
18	20	2.6	561	4	US-09-107-532A-3447
19	20	2.6	582	4	US-09-543-681A-2869
20	19	2.5	278866	4	US-09-949-016-13922
21	19	2.5	278866	4	US-09-949-016-13923
22	19	2.5	278866	4	US-09-949-016-13924
23	19	2.5	278866	4	US-09-949-016-13925
24	19	2.5	278866	4	US-09-949-016-13926
25	19	2.5	278866	4	US-09-949-016-14699
26	19	2.5	278866	4	US-09-949-016-14700
27	19	2.5	278866	4	US-09-949-016-14701

28	19	2.5	278866	4	US-09-949-016-14702	Sequence 14702, A
29	19	2.5	278866	4	US-09-949-016-14703	Sequence 14703, A
30	19	2.5	1230025	4	US-09-198-452A-1	Sequence 1, Appli
31	19	2.5	1230230	4	US-09-438-185A-1	Sequence 1, Appli
C 32	18	2.3	483	4	US-09-583-110-1501	Sequence 1501, Ap
33	18	2.3	741	4	US-09-134-000C-60	Sequence 60, Appl
34	18	2.3	915	4	US-09-328-352-2076	Sequence 2076, Ap
C 35	18	2.3	1221	2	US-08-934-846-3	Sequence 3, Appli
C 36	18	2.3	1221	3	US-09-238-557-3	Sequence 3, Appli
C 37	18	2.3	1254	3	US-08-934-846-1	Sequence 1, Appli
C 38	18	2.3	1254	3	US-09-238-557-1	Sequence 1, Appli
C 39	18	2.3	1419	4	US-09-543-681A-443	Sequence 443, App
40	18	2.3	2304	4	US-09-328-352-487	Sequence 487, App
41	18	2.3	7853	4	US-09-949-016-14067	Sequence 14067, A
42	18	2.3	129127	4	US-09-949-016-13481	Sequence 13481, A
C 43	18	2.3	767677	4	US-09-949-016-12147	Sequence 12147, A
C 44	18	2.3	767677	4	US-09-949-016-17361	Sequence 17361, A
45	17	2.2	320	3	US-09-030-607-224	Sequence 224, App

ALIGNMENTS

RESULT 1
US-09-292-412-1
; Sequence 1, Application US/09292412
; Patent No. 6432670
; GENERAL INFORMATION:
; APPLICANT: Payne, David
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: FAB I
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/292,412
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/790,043
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GMS0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-09-292-412-1

Query Match 100.0%; Score 771; DB 3; Length 771;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTTAAATCTTGAAAAAACAACATATGTCATCGGGAATCGCTAAATAAGCGTAGTATT 60
Db 1 ATGTTAAATCTTGAAAAAACAACATATGTCATCGGGAATCGCTAAATAAGCGTAGTATT 60
QY 61 GCTTTTGGTGCCTAAAGCTTTTGTAGTCAATAGGTGCTAAATAGTATTACTTTACCGT 120
Db 61 GCTTTTGGTGCCTAAAGCTTTTGTAGTCAATAGGTGCTAAATAGTATTACTTTACCGT 120
QY 121 AAAGAACGTAGCGGTAAAGAGCTTGAAAAATTTATAGAACAAATTAATCAACAGAGCG 180
Db 121 AAAGAACGTAGCGGTAAAGAGCTTGAAAAATTTATAGAACAAATTAATCAACAGAGCG 180
QY 181 CACTTATATCAAAATTCATGTTCAAGCGGATGAAGAGTTTAAATGGTTTTGAGCAAAATT 240
Db 181 CACTTATATCAAAATTCATGTTCAAGCGGATGAAGAGTTTAAATGGTTTTGAGCAAAATT 240
QY 241 GGTAAAGATGTTGGCAATATGATGGTGATATCATTCATTCGAATTCGCTTAATATGGAA 300
Db 241 GGTAAAGATGTTGGCAATATGATGGTGATATCATTCATTCGAATTCGCTTAATATGGAA 300
QY 301 GACTTACGGGAGCGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db 301 GACTTACGGGAGCGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
QY 361 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGT 420
Db 361 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGT 420
QY 421 AGCATTGTTGCAACAACATATTTAGGTGCGAAATTCGCAAGTTCAAAATTTAATATGTGATG 480
Db 421 AGCATTGTTGCAACAACATATTTAGGTGCGAAATTCGCAAGTTCAAAATTTAATATGTGATG 480
QY 481 GGTGTTGCTTAAAGCGAGCTTAGAACCAATGTTAAATTTAGCATTAGACTTAGGTCTCT 540
Db 481 GGTGTTGCTTAAAGCGAGCTTAGAACCAATGTTAAATTTAGCATTAGACTTAGGTCTCT 540
QY 541 GATAATATTTCCGGTTAATGCAATTTTCCAGTGGTCAATCCGTACATTAAGTGCAGAAAGGT 600
Db 541 GATAATATTTCCGGTTAATGCAATTTTCCAGTGGTCAATCCGTACATTAAGTGCAGAAAGGT 600
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QY 661 GTTGATCAAGTAGAGTAGTAAACAGCGGCTTACTTCTTAAAGTACATTATCAAGTGGC 720
Db 661 GTTGATCAAGTAGAGTAGTAAACAGCGGCTTACTTCTTAAAGTACATTATCAAGTGGC 720
QY 721 GTTACAGGTGAAAAATTTTCATGTAGATAGCGGATTCACGCAATTAATAAA 771
Db 721 GTTACAGGTGAAAAATTTTCATGTAGATAGCGGATTCACGCAATTAATAAA 771
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RESULT 2

US-09-292-411A-1

; Sequence 1, Application US/09292411A

; Patent No. 6753172

; GENERAL INFORMATION:

; APPLICANT: Lonsdale, John

; APPLICANT: Milner, Peter

; APPLICANT: Payne, David

; APPLICANT: Pearson, Stewart

; TITLE OF INVENTION: Fabi

; FILE REFERENCE: GM50005-D1

; CURRENT APPLICATION NUMBER: US/09/292,411A

; CURRENT FILING DATE: 1999-04-15

; PRIOR APPLICATION NUMBER: US 08/790,043

; PRIOR FILING DATE: 1997-01-28

; PRIOR APPLICATION NUMBER: US 60/024,845

; PRIOR FILING DATE: 1996-08-26

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

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; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-292-411A-1
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Query Match 100.0%; Score 771; DB 4; Length 771;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 771; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGTTAAATCTTGAAAAAACAACATATGTCATCGGGAATCGCTAAATAAGCGTAGTATT 60
Db 1 ATGTTAAATCTTGAAAAAACAACATATGTCATCGGGAATCGCTAAATAAGCGTAGTATT 60
QY 61 GCTTTTGGTGCCTAAAGCTTTTGTAGTCAATAGGTGCTAAATAGTATTACTTTACCGT 120
Db 61 GCTTTTGGTGCCTAAAGCTTTTGTAGTCAATAGGTGCTAAATAGTATTACTTTACCGT 120
QY 121 AAAGAACGTAGCGGTAAAGAGCTTGAAAAATTTATAGAACAAATTAATCAACAGAGCG 180
Db 121 AAAGAACGTAGCGGTAAAGAGCTTGAAAAATTTATAGAACAAATTAATCAACAGAGCG 180
QY 181 CACTTATATCAAAATTCATGTTCAAGCGGATGAAGAGTTTAAATGGTTTTGAGCAAAATT 240
Db 181 CACTTATATCAAAATTCATGTTCAAGCGGATGAAGAGTTTAAATGGTTTTGAGCAAAATT 240
QY 241 GGTAAAGATGTTGGCAATATGATGGTGATATCATTCATTCGAATTCGCTTAATATGGAA 300
Db 241 GGTAAAGATGTTGGCAATATGATGGTGATATCATTCATTCGAATTCGCTTAATATGGAA 300
QY 301 GACTTACGGGAGCGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db 301 GACTTACGGGAGCGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
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Db 361 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGT 420
QY 421 AGCATTGTTGCAACAACATATTTAGGTGCGCAATTTCCAGTGGTCAATCCGTACATTAAGTGCAGAAAGGT 480
Db 421 AGCATTGTTGCAACAACATATTTAGGTGCGCAATTTCCAGTGGTCAATCCGTACATTAAGTGCAGAAAGGT 480
QY 481 GGTGTTGCTTAAAGCGAGCTTAGAACCAATGTTAAATTTAGCATTAGACTTAGGTCTCT 540
Db 481 GGTGTTGCTTAAAGCGAGCTTAGAACCAATGTTAAATTTAGCATTAGACTTAGGTCTCT 540
QY 541 GATAATATTTCCGGTTAATGCAATTTTCCAGTGGTCAATCCGTACATTAAGTGCAGAAAGGT 600
Db 541 GATAATATTTCCGGTTAATGCAATTTTCCAGTGGTCAATCCGTACATTAAGTGCAGAAAGGT 600
QY 601 GTGGGTGGTTTCAATCAATTTCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAACGTAAAC 660
Db 601 GTGGGTGGTTTCAATCAATTTCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAACGTAAAC 660
QY 661 GTTGATCAAGTAGAGTAGTAAACAGCGGCTTACTTCTTAAAGTACATTATCAAGTGGC 720
Db 661 GTTGATCAAGTAGAGTAGTAAACAGCGGCTTACTTCTTAAAGTACATTATCAAGTGGC 720
QY 721 GTTACAGGTGAAAAATTTTCATGTAGATAGCGGATTCACGCAATTAATAAA 771
Db 721 GTTACAGGTGAAAAATTTTCATGTAGATAGCGGATTCACGCAATTAATAAA 771
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RESULT 3

US-10-138-701-5

; Sequence 5, Application US/10138701

; Patent No. 6753149

; GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc. et al.

; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides

; FILE REFERENCE: PB484

; CURRENT APPLICATION NUMBER: US/10/138,701

; CURRENT FILING DATE: 2002-05-06

; PRIOR APPLICATION NUMBER: US/09/512,255A

; PRIOR FILING DATE: 2000-02-24									
; PRIOR APPLICATION NUMBER: US 60/098,964									
; PRIOR FILING DATE: 1998-09-01									
; PRIOR APPLICATION NUMBER: US 60/009,861									
; PRIOR FILING DATE: 1996-01-05									
; PRIOR APPLICATION NUMBER: PCT/ US99/19726									
; PRIOR FILING DATE: 1999-08-31									
; PRIOR APPLICATION NUMBER: US 08/956,171									
; PRIOR FILING DATE: 1997-10-20									
; NUMBER OF SEQ ID NOS: 61									
; SOFTWARE: PatentIn version 3.0									
; SEQ ID NO 5									
; LENGTH: 916									
; TYPE: DNA									
; ORGANISM: Staphylococcus aureus									
US-10-138-701-5									
Query Match 65.6%; Score 506; DB 4; Length 916;									
Best Local Similarity 99.5%; Pred. No. 2.5e-247;									
Matches 656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;									
Qy	1	ATGTTAAATCTTGGAAAAACAAACATATGTCTCATATCGGAATCGCTAATAAGCGTAGTATT	60						
Db	96	ATGTTAAATCTTGGAAAAACAAACATATGTCTCATGGAATCGCTAATAAGCGTAGTATT	155						
Qy	61	GCCTTTTCGGTGTGCGTAAAGTTTTAGATCAATTAGGTGCTAAATAGTATTTCCTTACCGT	120						
Db	156	GCCTTTTCGGTGTGCGTAAAGTTTTAGATCAATTAGGTGCTAAATAGTATTTCCTTACCGT	215						
Qy	121	AAAGAACGTAGCCGCTAAAGAGCTTGGAAAAATATTAGAACAAATTAATCAACACGAAGCG	180						
Db	216	AAAGAACGTAGCCGCTAAAGAGCTTGGAAAAATATTAGAACAAATTAATCAACACGAAGCG	275						
Qy	181	CACCTTATATCAAAATGTATGTTTCAAGCGATCAAGAGGTTATTANTGGTTTGTAGCAATT	240						
Db	276	CACCTTATATCAAAATGTATGTTTCAAGCGATCAAGAGGTTATTANTGGTTTGTAGCAATT	335						
Qy	241	GGTAAAGATGTTGGCAATATTATGATGGTGTATATCATTCATTCGCATTTTGCTTAATATGAA	300						
Db	336	GGTAAAGATGTTGGCAATATTATGATGGTGTATATCATTCATTCGCATTTTGCTTAATATGAA	395						
Qy	301	GACTTACGCGGACGCTTTTCTGAAACTTCACGTGAAGGCTTCTTTGTAGCTCAAGACATT	360						
Db	396	GACTTACGCGGACGCTTTTCTGAAACTTCACGTGAAGGCTTCTTTGTAGCTCAAGACATT	455						
Qy	361	AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAATTAATTCGCAGAGGTGGT	420						
Db	456	AGTTCTTACTCATTTAAACAATTTGGCTCATGAAGCTAAAAATTAATTCGCAGAGGTGGT	515						
Qy	421	AGCATTTGCTCAACAACATATTTAGTGGCGCAATTCGCAGTTCAAAATTTAATGTGATG	480						
Db	516	AGCATTTGCTCAACAACATATTTAGTGGCGCAATTCGCAGTTCAAAATTTAATGTGATG	575						
Qy	481	GGTGTTCCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTTAGACTTAGGTCCT	540						
Db	576	GGTGTTCCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTTAGACTTAGGTCCT	635						
Qy	541	GATAAATATTCGCGTTAATGCAATTTACGTGGTCCAAATCCGTCATTTAAGTGCAAAAGGT	600						
Db	636	GATAAATATTCGCGTTAATGCAATTTACGTGGTCCAAATCCGTCATTTAAGTGCAAAAGGT	695						
Qy	601	GTGGGTGGTTTTCAATACAAATCTTTAAAGAAATCGAAGCGGTGCACCTTTAAAAACGTAA	659						
Db	696	GTGGGTGGTTTTCAATACAAATCTTTAAAGAAATCGAAGCGGTGCACCTTTAAAAACGTAA	754						

RESULT 4

US-08-956-171E-772
; Sequence 772, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
;

```

? Patrick S. Dillon
? Craig A. Rosen
? Steven C. Barash
? Michael R. Fannon
? TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
? NUMBER OF SEQUENCES: 5256
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Human Genome Sciences, Inc.
? STREET: 9410 Key West Avenue
? CITY: Rockville
? STATE: Maryland
? COUNTRY: USA
? ZIP: 20850
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
? COMPUTER: HP Vectra 486/33
? OPERATING SYSTEM: MSDOS version 6.2
? SOFTWARE: ASCII Text
?
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/956,171E
? FILING DATE: 20-Oct-1997
? CLASSIFICATION: <Unknown>
?
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 60/009,861
? FILING DATE: January 5, 1996
? APPLICATION NUMBER: 08/781,986
? FILING DATE: January 3, 1997
? ATTORNEY/AGENT INFORMATION:
? NAME: Mark J. Hyman
? REGISTRATION NUMBER: 46,789
? REFERENCE/DOCKET NUMBER: PB248P1
?
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (240) 314-1224
? TELEFAX: (301) 309-8439
?
? INFORMATION FOR SEQ ID NO: 772:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 704 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
?
? SEQUENCE DESCRIPTION: SEQ ID NO: 772:
?
? US-08-956-171E-772

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Query Match	56.7%	Score 437;	DB 4;	Length 704;
Best Local Similarity	99.6%	Pred. NO. 3.1e-212;		
Matches 537;	Conservative 0;	Mismatches 2;	Indels 0;	Gaps 0;
QY 1	ATGTTAAATCTTGAAACAAACATATGTCATCATGGAATCGCTAATAAGCGTAGTATT	60		
DB 24	ATGTTAAATCTTGAAACAAACATATGTCATCATGGAATCGCTAATAAGCGTAGTATT	83		
QY 61	GCCTTTGGTGCTCGCTAAAGTTTTAGATCAATTAGGTGCTAAATTTAGTATTTCCTTACCGT	120		
DB 84	GCCTTTGGTGCTCGCTAAAGTTTTAGATCAATTAGGTGCTAAATTTAGTATTTCCTTACCGT	143		
QY 121	AAAGAACGTAGCGCTAAAGAGCTTTGAAAAATTATTAGAACAAATTAATCAACACAGAAAGCG	180		
DB 144	AAAGAACGTAGCGCTAAAGAGCTTTGAAAAATTATTAGAACAAATTAATCAACACAGAAAGCG	203		
QY 181	CACCTTATACAAATTCATGTTTCAAGCGATGAAGAGTTTAAATGGTTTTGAGCAAAATT	240		
DB 204	CACCTTATACAAATTCATGTTTCAAGCGATGAAGAGTTTAAATGGTTTTGAGCAAAATT	263		
QY 241	GGTAAAGATGTTGGCAATATTGATGGTGATATCATTCATCGCATTTGCTAATATGGA	300		
DB 264	GGTAAAGATGTTGGCAATATTGATGGTGATATCATTCATCGCATTTGCTAATATGGA	323		
QY 301	GACCTTACGGCGAGCTTTTCTGAAACTTCACGTGAAGGCTTCTTTGTAGCTCAAGACATT	360		
DB 324	GACCTTACGGCGAGCTTTTCTGAAACTTCACGTGAAGGCTTCTTTGTAGCTCAAGACATT	383		
QY 361	AGTTCTTACTCATTAACAAATTTGGTGCTCATGAAGCTTAAAAAATTAATGCCAGAAAGTGCT	420		

Db 384 AGTCTTACTCATTAACAATTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGTGT 443
QY 421 AGCAATTTGCAACACATATTTAGTGGCGAATTCGCAATTCGCAATTAATATGATG 480
Db 444 AGCAATTTGCAACACATATTTAGTGGCGAATTCGCAATTCGCAATTAATATGATG 503
QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTAGCTTACGTC 539
Db 504 GGTGTTGCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTAGCTTACGTC 562

RESULT 5

US-08-781-986A-772
; Sequence 772, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512 772:
; INFORMATION FOR SEQ ID NO: 772:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear

US-08-781-986A-772

Query Match 56.7%; Score 437; DB 4; Length 704;
Best Local Similarity 99.6%; Pred. No. 3.1e-212;
Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAAACAAAACATATGTCATCATCGGAATCGCTAATAAGCGTAGTATT 60
Db 24 ATGTTAAATCTTGAAACAAAACATATGTCATCATCGGAATCGCTAATAAGCGTAGTATT 83
QY 61 GCTTTTGGTGCCTAAAGCTTTTAGATCAATTAGTGTCTAAATAGTATTACTTACCGT 120
Db 84 GCTTTTGGTGCCTAAAGCTTTTAGATCAATTAGTGTCTAAATAGTATTACTTACCGT 143
QY 121 AAAGACGTAGCGGTAAAGAGCTTGAAAAATATTAGAACAATTAATCAACACAGAGCG 180
Db 144 AAAGACGTAGCGGTAAAGAGCTTGAAAAATATTAGAACATTAATCAACACAGAGCG 203
QY 181 CACTTATATCAATTTGATGTTCAAGCGGATGAAGAGTTATTAAATGGTTTTCAGCAAAAT 240
Db 204 CACTTATATCAATTTGATGTTCAAGCGGATGAAGAGTTATTAAATGGTTTTCAGCAAAAT 263

QY 241 GGTAAAGATGTTGGCAATATTGATGCTGATATATCAATCGCATTTGCTAATATGAA 300
Db 264 GGTAAAGATGTTGGCAATATTGATGCTGATATATCAATCGCATTTGCTAATATGAA 323
QY 301 GACTTACCGGACGCGCTTTTCTGAAACTTCACGTGAAGCGTCTCTTGTAGCTCAAGACATT 360
Db 324 GACTTACCGGACGCGCTTTTCTGAAACTTCACGTGAAGCGTCTCTTGTAGCTCAAGACATT 383
QY 361 AGTCTTACTACTAATTAACAATTTGTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGTGT 420
Db 384 AGTCTTACTACTAATTAACAATTTGTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGTGT 443
QY 421 AGCAATTTGCAACACATATTTAGTGGCGAATTCGCAATTCGCAATTAATATGATG 480
Db 444 AGCAATTTGCAACACATATTTAGTGGCGAATTCGCAATTCGCAATTAATATGATG 503
QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTAGCTTACGTC 539
Db 504 GGTGTTGCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTAGCTTACGTC 562

RESULT 6

US-08-956-171E-514/c
; Sequence 514, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 514:

SEQUENCE CHARACTERISTICS:

LENGTH: 587 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 514:

US-08-956-171E-514

Query Match 8.2%; Score 63; DB 4; Length 587;
Best Local Similarity 100.0%; Pred. No. 5.5e-22;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 TTATCAAGTGGCGTTACAGGTGAAATATTTCATGTAGATAGCGGATTCCACGCAATTAAA 768
|||||
Db 547 TTATCAAGTGGCGTTACAGGTGAAATATTTCATGTAGATAGCGGATTCCACGCAATTAAA 488

QY 769 TAA 771
|||
Db 487 TAA 485

RESULT 7

US-08-781-986A-514/c
; Sequence 514, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/781,986A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Benson, Bob

; REGISTRATION NUMBER: 30,446

; REFERENCE/DOCKET NUMBER: PB248PP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 514:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 587 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-781-986A-514

Query Match 8.2%; Score 63; DB 4; Length 587;

Best Local Similarity 100.0%; Pred. No. 5.5e-22;

Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 709 TTATCAAGTGGCGTTACAGGTGAAATATTTCATGTAGATAGCGGATTCCACGCAATTAAA 768
|||||
Db 547 TTATCAAGTGGCGTTACAGGTGAAATATTTCATGTAGATAGCGGATTCCACGCAATTAAA 488

QY 769 TAA 771
|||
Db 487 TAA 485

RESULT 8

US-10-089-740-1
; Sequence 1, Application US/10089740
; Patent No. 6730684
; GENERAL INFORMATION:
; APPLICANT: Miller, William H.
; APPLICANT: Newlander, Kenneth A.

; APPLICANT: Seefeld, Mark A.
; APPLICANT: Uzinskas, Irene N.
; TITLE OF INVENTION: Fab I Inhibitors
; FILE REFERENCE: P51038
; CURRENT APPLICATION NUMBER: US/10/089,740
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 60/158,707
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-089-740-1

Query Match 3.9%; Score 30; DB 4; Length 39;

Best Local Similarity 100.0%; Pred. No. 3.4e-05;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACAAACAAACATATGTC 30
|||||
Db 10 ATGTTAAATCTTGAACAAACAAACATATGTC 39

RESULT 9

US-09-292-411A-3

; Sequence 3, Application US/09292411A

; Patent No. 6753172

; GENERAL INFORMATION:

; APPLICANT: Lonsdale, John

; APPLICANT: Milner, Peter

; APPLICANT: Payne, David

; APPLICANT: Pearson, Stewart

; TITLE OF INVENTION: FABI

; FILE REFERENCE: GMS0005-D1

; CURRENT APPLICATION NUMBER: US/09/292,411A

; CURRENT FILING DATE: 1999-04-15

; PRIOR APPLICATION NUMBER: US 08/790,043

; PRIOR FILING DATE: 1997-01-28

; PRIOR APPLICATION NUMBER: US 60/024,845

; PRIOR FILING DATE: 1996-08-26

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 39

; TYPE: DNA

; ORGANISM: Staphylococcus aureus

US-09-292-411A-3

Query Match 3.9%; Score 30; DB 4; Length 39;

Best Local Similarity 100.0%; Pred. No. 3.4e-05;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACAAACAAACATATGTC 30
|||||
Db 10 ATGTTAAATCTTGAACAAACAAACATATGTC 39

RESULT 10

US-10-089-739-1

; Sequence 1, Application US/10089739

; Patent No. 6762201

; GENERAL INFORMATION:

; APPLICANT: Miller, William H.

; APPLICANT: Newlander, Kenneth A.

; APPLICANT: Seefeld, Mark A.

; TITLE OF INVENTION: Fab I Inhibitors

; FILE REFERENCE: P51037

; CURRENT APPLICATION NUMBER: US/10/089,739

; CURRENT FILING DATE: 2002-08-20

; PRIOR APPLICATION NUMBER: 60/158,529

; PRIOR FILING DATE: 1999-10-08

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; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-089-739-1

Query Match          3.9%; Score 30; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 3.4e-05;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACAAACAAACATATGTC 30
    |||||
Db 10 ATGTTAAATCTTGAACAAACAAACATATGTC 39

RESULT 11
US-09-134-001C-1172
; Sequence 1172, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1172
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1172

Query Match          3.1%; Score 24; DB 3; Length 783;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 148 AAATTATTAGAACAAATTAATCAA 171
    |||||
Db 160 AAATTATTAGAACAAATTAATCAA 183

RESULT 12
US-10-089-740-4/c
; Sequence 4, Application US/10089740
; Patent No. 6730684
; GENERAL INFORMATION:
; APPLICANT: Miller, William H.
; APPLICANT: Newlander, Kenneth A.
; APPLICANT: Seefeld, Mark A.
; APPLICANT: Uzinskas, Irene N.
; TITLE OF INVENTION: Fab I Inhibitors
; FILE REFERENCE: P51038
; CURRENT APPLICATION NUMBER: US/10/089,740
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 60/158,707
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-089-740-4

Query Match          3.0%; Score 23; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTAATCTTGAACAAACAAACATA 26
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Db 23 TTAATCTTGAACAAACAAACATA 1

RESULT 13
US-10-089-739-4/c
; Sequence 4, Application US/10089739
; Patent No. 6762201
; GENERAL INFORMATION:
; APPLICANT: Miller, William H.
; APPLICANT: Newlander, Kenneth A.
; APPLICANT: Seefeld, Mark A.
; TITLE OF INVENTION: Fab I Inhibitors
; FILE REFERENCE: P51037
; CURRENT APPLICATION NUMBER: US/10/089,739
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/158,529
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-089-739-4

Query Match          3.0%; Score 23; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTAATCTTGAACAAACAAACATA 26
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Db 23 TTAATCTTGAACAAACAAACATA 1

RESULT 14
US-10-089-740-3
; Sequence 3, Application US/10089740
; Patent No. 6730684
; GENERAL INFORMATION:
; APPLICANT: Miller, William H.
; APPLICANT: Newlander, Kenneth A.
; APPLICANT: Seefeld, Mark A.
; APPLICANT: Uzinskas, Irene N.
; TITLE OF INVENTION: Fab I Inhibitors
; FILE REFERENCE: P51038
; CURRENT APPLICATION NUMBER: US/10/089,740
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 60/158,707
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-089-740-3

Query Match          2.7%; Score 21; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTAATCTTGAACAAACAAACATA 24
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Db 8 TTAATCTTGAACAAACAAACATA 28

RESULT 15
US-10-089-739-3
; Sequence 3, Application US/10089739
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTAATCTTGAACAAACAAACATA 26
    |||||
Db 23 TTAATCTTGAACAAACAAACATA 1

RESULT 13
US-10-089-739-4/c
; Sequence 4, Application US/10089739
; Patent No. 6762201
; GENERAL INFORMATION:
; APPLICANT: Miller, William H.
; APPLICANT: Newlander, Kenneth A.
; APPLICANT: Seefeld, Mark A.
; TITLE OF INVENTION: Fab I Inhibitors
; FILE REFERENCE: P51037
; CURRENT APPLICATION NUMBER: US/10/089,739
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/158,529
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-089-739-4

Query Match          3.0%; Score 23; DB 4; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTAATCTTGAACAAACAAACATA 26
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Db 23 TTAATCTTGAACAAACAAACATA 1

RESULT 14
US-10-089-740-3
; Sequence 3, Application US/10089740
; Patent No. 6730684
; GENERAL INFORMATION:
; APPLICANT: Miller, William H.
; APPLICANT: Newlander, Kenneth A.
; APPLICANT: Seefeld, Mark A.
; APPLICANT: Uzinskas, Irene N.
; TITLE OF INVENTION: Fab I Inhibitors
; FILE REFERENCE: P51038
; CURRENT APPLICATION NUMBER: US/10/089,740
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 60/158,707
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-089-740-3

Query Match          2.7%; Score 21; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTAATCTTGAACAAACAAACATA 24
    |||||
Db 8 TTAATCTTGAACAAACAAACATA 28

RESULT 15
US-10-089-739-3
; Sequence 3, Application US/10089739
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; Patent No. 6762201
; GENERAL INFORMATION:
; APPLICANT: Miller, William H.
; APPLICANT: Newlander, Kenneth A.
; APPLICANT: Seefeld, Mark A.
; TITLE OF INVENTION: Fab I Inhibitors
; FILE REFERENCE: P51037
; CURRENT APPLICATION NUMBER: US/10/089,739
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/158,529
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-089-739-3

Query Match 2.7%; Score 21; DB 4; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTAATCTTGAACAAACA 24
|||||
Db 8 TTAATCTTGAACAAACA 28

Search completed: September 6, 2005, 09:13:09
Job time : 143 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 6, 2005, 09:10:39 ; Search time 4728 Seconds
(without alignments)
1067.938 Million cell updates/sec

Title: US-08-790-043B-1
Perfect score: 771
Sequence: 1 ATGTTAAATCTTGAAACAA.....GATTCACCGCAATTAATAA 771

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 733684 seqs, 3274456166 residues

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Total number of hits satisfying chosen parameters: 14677368

Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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 - 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
 - 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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 - 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
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 - 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
 - 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
 - 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
 - 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
 - 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq.*
 - 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
 - 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
 - 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq.*
 - 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq.*
 - 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
 - 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq.*
 - 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq.*
 - 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq.*
 - 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq.*
 - 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq.*
 - 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq.*
 - 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq.*
 - 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
 - 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	720	93.4	771	17	US-10-282-122A-7734
3	720	93.4	771	21	US-10-857-625-263
4	720	93.4	6985	21	US-10-857-625-34
5	557	72.2	771	9	US-09-815-242-8794
6	506	65.6	916	16	US-10-138-701-5
7	506	65.6	916	20	US-10-823-785-5
					Sequence 1, Appli
					Sequence 7734, Ap
					Sequence 263, App
					Sequence 34, Appl
					Sequence 8794, Ap
					Sequence 5, Appli
					Sequence 5, Appli

RESULT 1
US-10-888-524-1
; Sequence 1, Application US/10888524
; Publication No. US20050112713A1
; GENERAL INFORMATION:
; APPLICANT: DEWOLF JR., WALTER E.
; APPLICANT: PAYNE, DAVID JOHN
; APPLICANT: MILNER, PETER HENRY
; APPLICANT: PEARSON, STEWART CAMPBELL
; APPLICANT: LONSDALE, JOHN TIMOTHY
; TITLE OF INVENTION: METHODS OF USING FAB I AND COMPOUNDS MODULATING FAB I ACTIVITY
; FILE REFERENCE: IPT-061.02
; CURRENT APPLICATION NUMBER: US/10/888,524
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/024,845
; PRIOR FILING DATE: 1996-08-28
; PRIOR APPLICATION NUMBER: 08/790,043
; PRIOR FILING DATE: 1997-08-28
; PRIOR APPLICATION NUMBER: 60/134,362
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 10/009,219
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: PCT/US00/12104
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

ALIGNMENTS

Sequence 1952, Ap
Sequence 1963, Ap
Sequence 4490, Ap
Sequence 4491, Ap
Sequence 772, App
Sequence 772, App
Sequence 1697, Ap
Sequence 3050, Ap
Sequence 4224, Ap
Sequence 5569, Ap
Sequence 1666, Ap
Sequence 4233, Ap
Sequence 4173, Ap
Sequence 8437, Ap
Sequence 2214, Ap
Sequence 2218, Ap
Sequence 2219, Ap
Sequence 2529, Ap
Sequence 3421, Ap
Sequence 4728, Ap
Sequence 4739, Ap
Sequence 4747, Ap
Sequence 5075, Ap
Sequence 5076, Ap
Sequence 3021, Ap
Sequence 5575, Ap
Sequence 514, App
Sequence 514, App
Sequence 2921, Ap
Sequence 5478, Ap
Sequence 3, Appli
Sequence 34355, A
Sequence 2044, Ap
Sequence 24707, A
Sequence 41051, A
Sequence 144, App
Sequence 6, Appli
Sequence 78598, A

Db 481 GGTGTTCTTAAGCGAGCTTAGAAGCAAAATGTTAAATATTATTAGCATTTAGACTTAGTGCCT 540
Qy 541 GATAAATATTCGCGTTAATGCAATTTAGCTGGTCCAAATCCGTACATTAAGTGCAAAAGGT 600
Db 541 GATAAATATTCGCGTTAATGCAATTTAGCTGGTCCAAATCCGTACATTAAGTGCAAAAGGT 600
Qy 601 GTGGTGGTTTCAATACAAATCTTAAAGAAATCGAAGAGCGTGCACTTTTAAACGTTAAC 660
Db 601 GTGGTGGTTTCAATACAAATCTTAAAGAAATCGAAGAGCGTGCACTTTTAAACGTTAAC 660
Qy 661 GTTGATCAAGTAGAAGTAGTAAACAGCGGCTTACTTCTTAAAGTGAAGTATCAAGTGGC 720
Db 661 GTTGATCAAGTAGAAGTAGTAAACAGCGGCTTACTTCTTAAAGTGAAGTATCAAGTGGC 720
Qy 721 GTTACAGGTGAAAATATTTCATGTAGATAGCGGATTCACGCAATTTAAATAA 771
Db 721 GTTACAGGTGAAAATATTTCATGTAGATAGCGGATTCACGCAATTTAAATAA 771

RESULT 3

US-10-857-625-263
; Sequence 263, Application US/10857625
; Publication No. US20050026189A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: MICROBIAL OPERONS
; FILE REFERENCE: ELITRA.036A
; CURRENT APPLICATION NUMBER: US/10/857,625
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/474768
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 833
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 263
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-857-625-263

Query Match 93.4%; Score 720; DB 21; Length 771;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 1 ATGTTAAATCTTGAAAACAAAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 60
Qy 61 GCTTTTGGTGCCTAAAGTTTATAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120
Db 61 GCTTTTGGTGCCTAAAGTTTATAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120
Qy 121 AAAGACGTAGCGTAAAGAGCTTGAAAATTTATAGAACAAATTAATCAACAGAGCG 180
Db 121 AAAGACGTAGCGTAAAGAGCTTGAAAATTTATAGAACAAATTAATCAACAGAGCG 180
Qy 181 CACTTATACAAATTGATGTTCAAAGCGATGAAGAGGTATTAAATGGTTTTGAGCAAAATT 240
Db 181 CACTTATACAAATTGATGTTCAAAGCGATGAAGAGGTATTAAATGGTTTTGAGCAAAATT 240
Qy 241 GGTAAAGATGTTGGCAATATTGATGGTGTATATCATTCATCGCATTTGCTAATATGGAA 300
Db 241 GGTAAAGATGTTGGCAATATTGATGGTGTATATCATTCATCGCATTTGCTAATATGGAA 300
Qy 301 GACTTACGGGAGCGCTTTTCTGAAAACCTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db 301 GACTTACGGGAGCGCTTTTCTGAAAACCTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Qy 361 AGTTCTTACTCATTAACAAATTGGGCTCATGAAGCTTAAATAATTAATGCCAGAGGTGGT 420
Db 361 AGTTCTTACTCATTAACAAATTGGGCTCATGAAGCTTAAATAATTAATGCCAGAGGTGGT 420

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Qy 481 GGTGTTGCTTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTATTAGCATTAGACTTAGTGCCT 540
Db 481 GGTGTTGCTTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTATTAGCATTAGACTTAGTGCCT 540
Qy 541 GATAATATTTCGGGTTAATGCAATTTTCAGCTGGTCCAAATCCGTACATTAAGTGCAAAAGGT 600
Db 541 GATAATATTTCGGGTTAATGCAATTTTCAGCTGGTCCAAATCCGTACATTAAGTGCAAAAGGT 600
Qy 601 GTGGTGGTTTCAATACAAATTTTAAAGAAATCGAAGAGCGTGCACTTTTAAACGTTAAC 660
Db 601 GTGGTGGTTTCAATACAAATTTTAAAGAAATCGAAGAGCGTGCACTTTTAAACGTTAAC 660
Qy 661 GTTGATCAAGTAGAAGTAGTAAACAGCGGCTTACTTCTTAAAGTGAAGTATCAAGTGGC 720
Db 661 GTTGATCAAGTAGAAGTAGTAAACAGCGGCTTACTTCTTAAAGTGAAGTATCAAGTGGC 720
Qy 721 GTTACAGGTGAAAATATTTCATGTAGATAGCGGATTCACGCAATTTAAATAA 771
Db 721 GTTACAGGTGAAAATATTTCATGTAGATAGCGGATTCACGCAATTTAAATAA 771

RESULT 4

US-10-857-625-34
; Sequence 34, Application US/10857625
; Publication No. US20050026189A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: MICROBIAL OPERONS
; FILE REFERENCE: ELITRA.036A
; CURRENT APPLICATION NUMBER: US/10/857,625
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/474768
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 833
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 6985
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-857-625-34

Query Match 93.4%; Score 720; DB 21; Length 6985;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 770; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ATGTTAAATCTTGAAAACAAAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 60
Db 6215 ATGTTAAATCTTGAAAACAAAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 6274
Qy 61 GCTTTTGGTGCCTAAAGTTTATAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120
Db 6275 GCTTTTGGTGCCTAAAGTTTATAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 6334
Qy 121 AAAGACGTAGCGTAAAGAGCTTGAAAATTTATAGAACAAATTAATCAACAGAGCG 180
Db 6335 AAAGACGTAGCGTAAAGAGCTTGAAAATTTATAGAACAAATTAATCAACAGAGCG 6394
Qy 181 CACTTATACAAATTGATGTTCAAAGCGATGAAGAGGTATTAAATGGTTTTGAGCAAAATT 240
Db 6395 CACTTATACAAATTGATGTTCAAAGCGATGAAGAGGTATTAAATGGTTTTGAGCAAAATT 6454
Qy 241 GGTAAAGATGTTGGCAATATTGATGGTGTATATCATTCATCGCATTTGCTAATATGGAA 300
Db 6455 GGTAAAGATGTTGGCAATATTGATGGTGTATATCATTCATCGCATTTGCTAATATGGAA 6514
Qy 301 GACTTACGGGAGCGCTTTTCTGAAAACCTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db 6515 GACTTACGGGAGCGCTTTTCTGAAAACCTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 6574

```
QY 361 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTTAAAAATTAATGCCAGAAGTGGT 420
Db |||||||
QY 421 AGCATTTGTTGCAACACATATTTAGTGGCGCAATTCGCAGTTTCAAAATTTAATATGTGATG 480
Db |||||||
QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAATTTGTAATATTTAGCATTAGACTTAGTCTCT 540
Db |||||||
QY 541 GATAATATTCGGTGTAAATCAATTTTCAGCTGGTCCAAATCCGTACATTAAGTGCAAAAAGGT 600
Db |||||||
QY 601 GTGGTGGTGGTTTCAATACAATTTCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAAGCTAAC 660
Db |||||||
QY 661 GTTGATCAAGTAGAAGTAGGTAACAGCGGCTTACTTCTTAAAGTGAATTAATCAAGTGGC 720
Db |||||||
QY 721 GTTACAGTGAAATTAATTCATGTAGATAGCGGATTCACGCAATTAATAAA 771
Db |||||||
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RESULT 5

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US-09-815-242-8794
; Sequence 8794, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8794
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(771)
US-09-815-242-8794
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Query Match 72.2%; Score 557; DB 9; Length 771;
Best Local Similarity 99.7%; Pred. No. 1.3e-268;
Matches 557; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACCAAAACATATGTCATCATGGAATCGCTTAATAAGCGTAGTATT 60
Db |||||||
QY 61 GCTTTTGGTGTGCGTAAAGATTTTAGATCAATTTAGTGTCTAAATTTAGTATTACTTTACCGT 120
Db |||||||
QY 121 AAAGAACCTAGCCGTAAAGAGCTTGAAGAAATTTTAGAACCAATTTAAATCAACCAAGACG 180
Db |||||||
QY 181 CACTTATATCAAAATGATGTTCAAAGCGATGAAGAGGTTTAAATGTTTGGAGCAAAAT 240
Db |||||||
QY 241 GGTAAAGATGTTGGCAATATTTGATGGTGTATATCAATTCGCAATTTGCTAAATATGGA 300
Db |||||||
QY 301 GACTTACCGGACGCTTTTCTGAAACTTCAGCTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db |||||||
QY 361 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTTAAAGAAATTAATGCCAGAAGTGGT 420
Db |||||||
QY 421 AGCATTTGTTGCAACACATATTTAGTGGCGCAATTCGCAGTTTCAAAATTTAATATGTGATG 480
Db |||||||
QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAATTTGTAATATTTAGCATTAGACTTAGTCTCT 540
Db |||||||
QY 541 GATAATATTCGGTGTAAATCAATTTTCAGCTGGTCCAAATCCGTACATTAAGTGCAAAAAGGT 600
Db |||||||
QY 601 GTGGTGGTGGTTTCAATACAATTTCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAAGCTAA 659
Db |||||||

RESULT 6
US-10-138-701-5
; Sequence 5, Application US/10138701
; Publication No. US20030186364A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
; FILE REFERENCE: PB484
; CURRENT APPLICATION NUMBER: US/10/138,701
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US/09/512,255A
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/098,964
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-05
; PRIOR APPLICATION NUMBER: PCT/ US99/19726
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 5
; LENGTH: 916
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; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-138-701-5

Query Match      65.6%; Score 506; DB 16; Length 916;
Best Local Similarity 99.5%; Pred. No. 5.1e-243;
Matches 656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACACAAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 60
Db ATGTTAAATCTTGAACACAAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 155

QY 61 GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120
Db GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 215

QY 121 AAAGAACGTAGCCGTAAAGAGCTTGAAGAAATTAATTAGAACAAATTAATAACACAGAGCG 180
Db AAAGAACGTAGCCGTAAAGAGCTTGAAGAAATTAATTAGAACAAATTAATAACACAGAGCG 275

QY 181 CACTTATATCAAAATTGATGTTCAAAGCGATGAAGGTTAATATGTTTGTAGCAAAAT 240
Db CACTTATATCAAAATTGATGTTCAAAGCGATGAAGGTTAATATGTTTGTAGCAAAAT 335

QY 241 GGTAAAGATGTTGCAATATGATGTTGATATCATTCATCGCATTTGCTAATATGGAA 300
Db GGTAAAGATGTTGCAATATGATGTTGATATCATTCATCGCATTTGCTAATATGGAA 395

QY 301 GACTTACCGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db GACTTACCGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 455

QY 361 AGTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 420
Db AGTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 515

QY 421 AGCATTTGTCACACACATATTTAGTGGCGAATTCGCAGTTCAAAATTAATATGTATG 480
Db AGCATTTGTCACACACATATTTAGTGGCGAATTCGCAGTTCAAAATTAATATGTATG 575

QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAATGTTAAATATTTAGCATTTAGCTTAGTCCT 540
Db GGTGTTGCTAAAGCGAGCTTAGAAGCAATGTTAAATATTTAGCATTTAGCTTAGTCCT 635

QY 541 GATAATATTCGCTTAATCAATTTTCAGTGGTCCAATCCGTCACATTAAGTGCAAAAGGT 600
Db GATAATATTCGCTTAATCAATTTTCAGTGGTCCAATCCGTCACATTAAGTGCAAAAGGT 695

QY 601 GTGGGTGGTTTCAATACAAATCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAACGTAA 659
Db GTGGGTGGTTTCAATACAAATCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAACGTAA 754

RESULT 7
US-10-823-785-5
; Sequence 5, Application US/10823785
; Publication No. US20040265962A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
; FILE REFERENCE: PB484
; CURRENT APPLICATION NUMBER: US/10/823,785
; PRIORITY FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/512,255
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/098,964
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-05
; PRIOR APPLICATION NUMBER: PCT/US99/19726
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
```

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; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-823-785-5

Query Match      65.6%; Score 506; DB 20; Length 916;
Best Local Similarity 99.5%; Pred. No. 5.1e-243;
Matches 656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACACAAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 60
Db ATGTTAAATCTTGAACACAAAACATATGTCATCATGCGGAATCGCTAATAAGCGTAGTATT 155

QY 61 GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120
Db GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 215

QY 121 AAAGAACGTAGCCGTAAAGAGCTTGAAGAAATTAATTAGAACAAATTAATAACACAGAGCG 180
Db AAAGAACGTAGCCGTAAAGAGCTTGAAGAAATTAATTAGAACAAATTAATAACACAGAGCG 275

QY 181 CACTTATATCAAAATTCATGTTCAAAGCGATGAAGGTTAATATGTTTGTAGCAAAAT 240
Db CACTTATATCAAAATTCATGTTCAAAGCGATGAAGGTTAATATGTTTGTAGCAAAAT 335

QY 241 GGTAAAGATGTTGGCAATATTCATGTTGATATCATTCATCGCATTTGCTAATATGGAA 300
Db GGTAAAGATGTTGGCAATATTCATGTTGATATCATTCATCGCATTTGCTAATATGGAA 395

QY 301 GACTTACCGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
Db GACTTACCGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 455

QY 361 AGTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 420
Db AGTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAGTGGT 515

QY 421 AGCATTTGTCACACACATATTTAGTGGCGAATTCGCAGTTCAAAATTAATATGTATG 480
Db AGCATTTGTCACACACATATTTAGTGGCGAATTCGCAGTTCAAAATTAATATGTATG 575

QY 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAATGTTAAATATTTAGCATTTAGCTTAGTCCT 540
Db GGTGTTGCTAAAGCGAGCTTAGAAGCAATGTTAAATATTTAGCATTTAGCTTAGTCCT 635

QY 541 GATAATATTCGCTTAATCAATTTTCAGTGGTCCAATCCGTCACATTAAGTGCAAAAGGT 600
Db GATAATATTCGCTTAATCAATTTTCAGTGGTCCAATCCGTCACATTAAGTGCAAAAGGT 695

QY 601 GTGGGTGGTTTCAATACAAATCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAACGTAA 659
Db GTGGGTGGTTTCAATACAAATCTTAAAGAAATCGAAGAGCGTGCACCTTTAAAAACGTAA 754

RESULT 8
US-09-815-242-1952/c
; Sequence 1952, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; PROKARYOTES
; FILE REFERENCE: ELITRA.011A
```



```

: APPLICANT: Haselbeck, Robert
: APPLICANT: Ohlsen, Kari
: APPLICANT: Zyskind, Judith
: APPLICANT: Wall, Daniel
: APPLICANT: Trawick, John
: APPLICANT: Carr, Grant
: APPLICANT: Yamamoto, Robert
: APPLICANT: Forsyth, R.
: APPLICANT: Xu, H.
: TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
: FILE REFERENCE: ELITRA.034A
: CURRENT APPLICATION NUMBER: US/10/282,122A
: CURRENT FILING DATE: 2003-02-20
: PRIOR FILING DATE: 60/191,078
: PRIOR FILING DATE: 2000-03-21
: PRIOR APPLICATION NUMBER: 60/206,848
: PRIOR FILING DATE: 2000-05-23
: PRIOR APPLICATION NUMBER: 60/207,727
: PRIOR FILING DATE: 2000-05-26
: PRIOR APPLICATION NUMBER: 60/230,335
: PRIOR FILING DATE: 2000-09-06
: PRIOR APPLICATION NUMBER: 60/230,347
: PRIOR FILING DATE: 2000-09-09
: PRIOR APPLICATION NUMBER: 60/242,578
: PRIOR FILING DATE: 2000-10-23
: PRIOR APPLICATION NUMBER: 60/253,625
: PRIOR FILING DATE: 2000-11-27
: PRIOR APPLICATION NUMBER: 60/257,931
: PRIOR FILING DATE: 2000-12-22
: PRIOR APPLICATION NUMBER: 60/267,636
: PRIOR FILING DATE: 2001-02-09
: PRIOR APPLICATION NUMBER: 60/269,308
: PRIOR FILING DATE: 2001-02-16
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 78614
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 4490
: LENGTH: 552
: TYPE: DNA
: ORGANISM: Staphylococcus aureus
US-10-282-122A-4490

```

Query Match	59.1%;	Score 456;	DB 17;	Length 552;
Best Local Similarity	100.0%;	Pred. No. 5.9e-218;		
Matches 456;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	ATGTTAAATCTTGAAGAACAAACACATATGTCATCATCGGAATCGCTAAATACGCGTAGTATT	60	
Db	456	ATGTTAAATCTTGAAGAACAAACACATATGTCATCATCGGAATCGCTAAATACGCGTAGTATT	397	
Qy	61	GCTTTTGGTGTGCGCTAAAGTTTTAGATCAATTTAGGTGCTAAATTTAGTATTTTTACTTACCGT	120	
Db	396	GCTTTTGGTGTGCGCTAAAGTTTTAGATCAATTTAGGTGCTAAATTTAGTATTTTTACTTACCGT	337	
Qy	121	AAAGACGTAGCCGTAAAGAGCTTTGAAAAATTTATAGAACAAATTTAAATCAACACGAGCG	180	
Db	336	AAAGACGTAGCCGTAAAGAGCTTTGAAAAATTTATAGAACAAATTTAAATCAACACGAGAGCG	277	
Qy	181	CACTTATATCAAAATTGATGTTTCAAAGCGCATGAAGAGGTTATTAATGGTTTTGAGCAAAATT	240	
Db	276	CACTTATATCAAAATTGATGTTTCAAAGCGCATGAAGAGGTTATTAATGGTTTTGAGCAAAATT	217	
Qy	241	GGTAAAGATGTTGGCAATATTTGATGGTGGTATATCATTCATTCGCAATTTGCTTAATATGGAA	300	
Db	216	GGTAAAGATGTTGGCAATATTTGATGGTGGTATATCATTCATTCATTCGCAATTTGCTTAATATGGAA	157	
Qy	301	GACTTACGCGGACGCTTTTCTGAAACTTCACGTCAAGGCTTCTTGGTTAGCTCAAGACATT	360	
Db	156	GACTTACGCGGACGCTTTTCTGAAACTTCACGTCAAGGCTTCTTGGTTAGCTCAAGACATT	97	
Qy	361	AGTTCTTATCTAATTAACAATTTGTGGCTCATGAAGCTAAAAAATTTAATGCCAAGAAGGTGGT	420	
Db	96	AGTTCTTATCTAATTAACAATTTGTGGCTCATGAAGCTAAAAAATTTAATGCCAAGAAGGTGGT	37	

Qy 421 AGCATTGTTGCACCAACATATTTAGTGGCGGAATTC 456
|||
Db 36 AGCATTGTTGCACCAACATATTTAGTGGCGGAATTC 1

RESULT 11
US-10-282-122A-4491/c
; Sequence 4491, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4491
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-282-122A-4491

	Query Match	59.1%;	Score 456;	DB 17;	Length 552;
	Best Local Similarity	100.0%;	Prod. No. 5.9e-218;		
	Matches 456;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ATGCTTAAATCTTCGAAACAAAACATATGT	CATCATGCGAATCGCTAATAAGCGTAGTATT	60	
Db	456	ATGCTTAAATCTTCGAAACAAAACATATGT	CATCATGCGAATCGCTAATAAGCGTAGTATT	397	
QY	61	GCCTTTTGGTGTCCTAAAGCTTTAGATCAAT	TAGTGCTAAATAGTATTATCTTACCGT	120	
Db	396	GCCTTTTGGTGTCCTAAAGCTTTAGATCAAT	TAGTGCTAAATAGTATTATCTTACCGT	337	
QY	121	AAGAGACGTAGCGTAAGAGCGTTGAAAATTA	TATAGACAAATTAATCAACACAGAGCG	180	
Db	336	AAGAGACGTAGCGTAAGAGCGTTGAAAATTA	TATAGACAAATTAATCAACACAGAGCG	277	
QY	181	CACCTTATATCAAAATTCGATGTTCAAAGCG	ATGAAGAGGTATTAAATGGTTTTGAGCAAAATT	240	

276	Db	CACTTATATCAAATTGATGTTCAAGCGATGAAGGTTATTAAATGGTTTTGAGCAAAATT	217
241	QY	GGTAAAGATGTTGGCAATATTGATGGTGATATCATTCGAATTCGTAATATGGAA	300
216	Db	GGTAAAGATGTTGGCAATATTGATGGTGATATCATTCGAATTCGTAATATGGAA	157
301	QY	GACTTTACGGCGGACGCTTTTCTGAAACTTCACGTGAAGCTTCTTGTTAGCTCAAGACATT	360
156	Db	GACTTTACGGCGGACGCTTTTCTGAAACTTCACGTGAAGCTTCTTGTTAGCTCAAGACATT	97
361	QY	AGTCTTACTCATTTAAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAAAGTGGT	420
96	Db	AGTCTTACTCATTTAAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAAAGTGGT	37
421	QY	AGCATTGTTGGCAACAACATATTTAGTGGCGCAATTC	456
36	Db	AGCATTGTTGGCAACAACATATTTAGTGGCGCAATTC	1

```

RESULT 12
US-08-781-986A-772
; Sequence 772, Application US/08781986A
; Publication No. US2003005436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 772:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-772

```

	Query Match	Best Local Similarity	Score 437;	DB 8;	Length 704;
	Matches 537;	Conservative	0;	Mismatches 2;	Indels 0;
	Gaps 0				
Qy	1	ATGTTAAATCTTGGAAAACAAAACATATGTCATCATCGGAATCGCTAATAAGCGGTAGTATT	60		
Db	24	ATGTTAAATCTTGGAAAACAAAACATATGTCATCATCGGAATCGCTAATAAGCGGTAGTATT	83		
Qy	61	GCCTTTGGTGCCTAAAGTTTTAGATCAATATTAGTGCTAAATTAGTATTACTTACCGT	120		
Db	84	GCCTTTGGTGCCTAAAGTTTTAGATCAATTTGGTGTCTAAATTAGTATTACTTACCGT	143		

Qy	121	AAAGACGTAGCGTAAAGAGCTTGAAAAATTTATTAGAACAATTAATAATCAACGGAAGCG	180
Dd	144	AAAGAACGTAGCGTAAAGAGCTTGAAAAATTTATTAGAACAATTAATAATCAACGGAAGCG	203
Qy	181	CAC TTATATCAAATTCATGTTCCAAAGCGATGAAGAGGTTATTAAATGGTTTTGAGCAAAAT	240
Dd	204	CAC TTATATCAAATTCATGTTCCAAAGCGATGAAGAGGTTATTAAATGGTTTTGAGCAAAAT	263
Qy	241	GGTAAAGATGTTGGCAATATTCATGGTGTATATCATTCATCGCAATTTGCTAATAATGAAA	300
Dd	264	GGTAAAGATGTTGGCAATATTCATGGTGTATATCATTCATCGCAATTTGCTAATAATGAAA	323
Qy	301	GACTTAGCGGACGCCTTTTCTGAACCTCAGTGAAGGCTTCTGTTAGCTCAAGACATTT	360
Dd	324	GACTTAGCGGACGCCTTTTCTGAACCTCAGTGAAGGCTTCTGTTAGCTCAAGACATTT	383
Qy	361	AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAGAGGTGGT	420
Dd	384	AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAGAGGTGGT	443
Qy	421	AGCATTTGTTGCAACACATATTTAGTGGCGAATTCGCAGTTTCAAAAATTAATAATGTGATG	480
Dd	444	AGCATTTGTTGCAACACATATTTAGTGGCGAATTCGCAGTTTCAAAAATTAATAATGTGATG	503
Qy	481	GGTGTGCTTAAGCGAGCTTAGAACAATGTTAAATTTAGCAATTTAGACTTAGACTTAGGTCC	539
Dd	504	GGTGTGCTTAAGCGAGCTTAGAACAATGTTAAATTTAGCAATTTAGACTTAGACTTAGGTCC	562

RESULT 13

US-10-329-624-772

; Sequence 772, Application US/10329624

; Publication No. US20040043037A1

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; Gil H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/329,624

; FILING DATE: 27-Dec-2002

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/956,171

; FILING DATE: October 20, 1997

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248PID1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 772:


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 772:
US-10-329-624-772

Query Match          56.7%; Score 437; DB 18; Length 704;
Best Local Similarity 99.6%; Pred. No. 2.1e-208;
Matches 537; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGTTAAATCTTGAACAAACAAACATATGTCATCATGCGAATCGCTAATAAGCGTAGTATT 60
DB 24 ATGTTAAATCTTGAACAAACAAACATATGTCATCATGCGAATCGCTAATAAGCGTAGTATT 83
QY 61 GCTTTTGGTGTGCTAAAGTTTTAGATCAATAGGTGCTAAATTAGTATTACTTACCGT 120
DB 84 GCTTTTGGTGTGCTAAAGTTTTAGATCAATAGGTGCTAAATTAGTATTACTTACCGT 143
QY 121 AAGAAAGCTAGCCGTGAAGAGCTTTGAAAAATTTAGAACAAATTAATCAACCAAGAGCG 180
DB 144 AAGAAAGCTAGCCGTGAAGAGCTTTGAAAAATTTAGAACAAATTAATCAACCAAGAGCG 203
QY 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGTTAATTAATGGTTTTGAGCAAAAT 240
DB 204 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGTTAATTAATGGTTTTGAGCAAAAT 263
QY 241 GGTAAAGATGTTGGCAATATGATGTTCAAGCGATGAAGAGTTAATTAATGGTTTTGAGCA 300
DB 264 GGTAAAGATGTTGGCAATATGATGTTCAAGCGATGAAGAGTTAATTAATGGTTTTGAGCA 323
QY 301 GACTTACGCGAGCGCTTTTCTGAAACTTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
DB 324 GACTTACGCGAGCGCTTTTCTGAAACTTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 383
QY 361 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGT 420
DB 384 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGT 443
QY 421 AGCATTTGTCACACACATATTTAGTGGCGAATTCGCGATTCGCAATTAATATATATGATG 480
DB 444 AGCATTTGTCACACACATATTTAGTGGCGAATTCGCGATTCGCAATTAATATATGATG 503
QY 481 GGTGTTGCTTAAGCGAGCTTTAGAACAAATGTTAAATATTAGCATTAGACTTAGTGCC 539
DB 504 GGTGTTGCTTAAGCGAGCTTTAGAACAAATGTTAAATATTAGCATTAGACTTAGTGCC 562

RESULT 14
US-09-815-242-1697/c
; Sequence 1697, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26

Query Match          42.0%; Score 324; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 9.5e-152;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 135 TAAAGAGCTTTGAAAAATTTAGAACAAATTAATTAATGGTTTTGAGCAAAATTTGGTAAAGATGTTGG 194
DB 324 TAAAGAGCTTTGAAAAATTTAGAACAAATTAATTAATGGTTTTGAGCAAAATTTGGTAAAGATGTTGG 265
QY 195 TGATGTTCAAAAGCGATGAAGAGTTAATTAATGGTTTTGAGCAAAATTTGGTAAAGATGTTGG 254
DB 264 TGATGTTCAAAAGCGATGAAGAGTTAATTAATGGTTTTGAGCAAAATTTGGTAAAGATGTTGG 205
QY 255 CAATATTGATGTTGATATATCAATTCATTCGATTCGATTAATGCGAATTTGCTTAATGGAAGACTTAGCGGACG 314
DB 204 CAATATTGATGTTGATATATCAATTCATTCGATTCGATTAATGCGAATTTGCTTAATGGAAGACTTAGCGGACG 145
QY 315 CTTTCTGAAACTTTCACGTGAAGGCTTCTTGTAGCTCAAGCATTAGTTCTTACTCAAT 374
DB 144 CTTTCTGAAACTTTCACGTGAAGGCTTCTTGTAGCTCAAGCATTAGTTCTTACTCAAT 85
QY 375 ACAAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGTAGCATTTGTTGCAAC 434
DB 84 ACAAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGTAGCATTTGTTGCAAC 25
QY 435 AACATATTTAGTGGCGAATTCGC 458
DB 24 AACATATTTAGTGGCGAATTCGC 1

RESULT 15
US-09-815-242-3050/c
; Sequence 3050, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3050
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-815-242-3050

Query Match 42.0%; Score 324; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 9.5e-152; Indels 0; Gaps 0;
Matches 324; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 135 TAAAGAGCTTGA AAAATTATTAGAACAAATTAATCAACCAAGCGCAGCTTATATCAAAAT 194
DB 324 TAAAGAGCTTGA AAAATTATTAGAACAAATTAATCAACCAAGCGCAGCTTATATCAAAAT 265
QY 195 TGATGTTCAAGCGGATGAAGAGGTTATTAAATGGTTTGGAGCAAAATGGTAAAGATGTTGG 254
DB 264 TGATGTTCAAGCGGATGAAGAGGTTATTAAATGGTTTGGAGCAAAATGGTAAAGATGTTGG 205
QY 255 CAATATTGATGGTATATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 314
DB 204 CAATATTGATGGTATATCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTCATTC 145
QY 315 CTTTCTGAACTTCACGTTGAAGGCTTCTTGTAGCTCAAGACATTAGTTCTTACTCATT 374
DB 144 CTTTCTGAACTTCACGTTGAAGGCTTCTTGTAGCTCAAGACATTAGTTCTTACTCATT 85
QY 375 AACAAATTGGGCTCATGAAGCTAA AAAAATTAATGCCAGAGGTTAGCATTTGTTGCAAC 434
DB 84 AACAAATTGGGCTCATGAAGCTAA AAAAATTAATGCCAGAGGTTAGCATTTGTTGCAAC 25
QY 435 AACATATTTAGTGGCGAATTCGC 458
DB 24 AACATATTTAGTGGCGAATTCGC 1

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Job time : 4732 secs

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Run on: September 6, 2005, 09:13:03 ; Search time 182 Seconds
(without alignments)

2301.576 Million cell updates/sec

Title:

US-08-790-043B-2

Perfect score: 256

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

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Word size: 1

Total number of hits satisfying chosen parameters: 2399978

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=arni -MINMATCH=0 1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	256	100.0	771	3	US-09-292-412-1
2	256	100.0	771	4	US-09-292-412-1
3	190	74.2	916	4	US-10-138-701-5
4	159	62.1	704	4	US-08-956-171B-772
5	159	62.1	704	4	US-08-781-986A-772
6	33	12.9	587	4	US-08-956-171B-514
7	33	12.9	587	4	US-08-781-986A-514
8	32	12.5	783	3	US-09-134-001C-1172
9	14	5.5	906	4	US-09-540-236-500
10	14	5.5	912	4	US-09-328-352-4085
11	14	5.5	65792	4	US-09-596-002-31
12	14	5.5	1830121	4	US-09-557-884-1

ALIGNMENTS

RESULT 1
US-09-292-412-1
; Sequence 1, Application US/09292412
; Patent No. 6432670
; GENERAL INFORMATION:
; APPLICANT: Payne, David
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: FAB I
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dechert Price & Rhoads
; STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
; CITY: Philadelphia
; STATE: PA
; COUNTRY: US
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION NUMBER: US/09/292,412
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/790,043
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Falk, Stephen T
; REGISTRATION NUMBER: 36,795
; REFERENCE/DOCKET NUMBER: GMS0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-994-2488

```
; TELEFAX: 215-994-2222
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-292-412-1

Alignment Scores:
Pred. No.: 3,64e-272 Length: 771
Score: 256.00 Matches: 256
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-292-412-1 (1-771)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
DB 1 ATGTTAAATCTTGAACCAACAAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 60

QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
DB 61 GCTTTTGGTGTGCTAAAGCTTTTAGTCAATTAGGTGCTAAATTAGTATTACTTACCGT 120

QY 41 LysGluArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAla 60
DB 121 AAAGAACGTAGCGGTAAAGAGCTTGAAAAATATTAGAACAAATTAATAACACAGAGCG 180

QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
DB 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGGTTATTAAATGGTTTCAGCAAAAT 240

QY 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
DB 241 GGTAAAGATGTTGGCAATATGATGGTGTATATCATTCAATCGCATTTGCTTAATATGNA 300

QY 101 AspLeuArgGlyArgPheSerGluThrSerArgGlyGlyPheLeuLeuAlaGlnAspIle 120
DB 301 GACTTACGGGACGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360

QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGly 140
DB 361 AGTTCCTACTCAATTAACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGT 420

QY 141 SerIleValAlaThrTyrLeuGlyGlyPheAlaValGlnAsnTyrAsnValMet 160
DB 421 AGCATTTGTCACCAACATATTTAGTGGCGAATTCGCAGTTCAAAATTTAATATGTGATG 480

QY 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
DB 481 GGTGTGTCTAAAGCGAGCTTAGAAGCAATGTTAAATATTAGCATTTAGCTTAGTCTCT 540

QY 181 AspAsnIleArgValAsnAlaIleSerAlaGlyProIleArgThrLeuSerAlaLysGly 200
DB 541 GATAATATTCGGGTAAATCAATTTAGCTGTCAATCCGACATTAAAGTCAAAAAGGT 600

QY 201 ValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAsn 220
DB 601 GTGGGTGGTTTCAATACATTTCTTAAGAAATCGAAGCGTGCACCTTTAAAAAGTAAAC 660

QY 221 ValAspGlnValGluValGlyLysThrAlaLysTyrLeuLeuSerAspLeuSerGly 240
DB 661 GTTGATCAAGTAGAAGTAGGTAAAAACAGCGGCTTACTTTRTTAAGTCACTTATCAAGTGGC 720

QY 241 ValThrGlyLysIleHisValAspSerGlyPheHisAlaIleIys 256
DB 721 GTTACAGGTGAATAATATTATCATGTAGATACGGATTCCACGCAATTAATA 768
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US-09-292-411A-1
; Sequence 1, Application US/09292411A
; Patent No. 6753172
; GENERAL INFORMATION:
; APPLICANT: Lonsdale, John
; APPLICANT: Milner, Peter
; APPLICANT: Payne, David
; APPLICANT: Pearson, Stewart
; TITLE OF INVENTION: FdBI
; FILE REFERENCE: GMS0005-D1
; CURRENT APPLICATION NUMBER: US/09/292,411A
; CURRENT FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: US 08/790,043
; PRIOR FILING DATE: 1997-01-28
; PRIOR APPLICATION NUMBER: US 60/024,845
; PRIOR FILING DATE: 1996-08-26
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-09-292-411A-1

Alignment Scores:
Pred. No.: 3,64e-272 Length: 771
Score: 256.00 Matches: 256
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-292-411A-1 (1-771)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
DB 1 ATGTTAAATCTTGAACCAACAAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 60

QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
DB 61 GCTTTTGGTGTGCTAAAGCTTTTAGTCAATTAGGTGCTAAATTAGTATTACTTACCGT 120

QY 41 LysGluArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAla 60
DB 121 AAAGAACGTAGCGGTAAAGAGCTTGAAAAATATTAGAACAAATTAATAACACAGAGCG 180

QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
DB 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGGTTATTAAATGGTTTCAGCAAAAT 240

QY 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
DB 241 GGTAAAGATGTTGGCAATATTTAGTGGTGTATATCATTCAATCGCATTTGCTTAATATGNA 300

QY 101 AspLeuArgGlyArgPheSerGluThrSerArgGlyGlyPheLeuLeuAlaGlnAspIle 120
DB 301 GACTTACGGGACGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360

QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGly 140
DB 361 AGTTCCTACTCAATTAACAATTTGGCTCATGAAGCTTAAAAAATTAATGCCAAGGTGGT 420

QY 141 SerIleValAlaThrTyrLeuGlyGlyPheAlaValGlnAsnTyrAsnValMet 160
DB 421 AGCATTTGTCACCAACATATTTAGTGGCGAATTCGCAGTTCAAAATTTAATATGTGATG 480

QY 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
DB 481 GGTGTGTCTAAAGCGAGCTTAGAAGCAATGTTAAATATTAGCATTTAGCTTAGTCTCT 540

QY 181 AspAsnIleArgValAsnAlaIleSerAlaGlyProIleArgThrLeuSerAlaLysGly 200
DB 541 GATAATATTCGGGTAAATGCAATTTTCAGTGGTCCAAATTCGAGGTTCAAAATTTAATATGTGATG 480

QY 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
DB 481 GGTGTGTCTAAAGCGAGCTTAGAAGCAATGTTAAATATTAGCATTTAGCTTAGTCTCT 540

QY 181 AspAsnIleArgValAsnAlaIleSerAlaGlyProIleArgThrLeuSerAlaLysGly 200
DB 541 GATAATATTCGGGTAAATGCAATTTTCAGTGGTCCAAATTCGAGGTTCAAAATTTAATATGTGATG 480
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;
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 772:
US-08-956-171E-772

Alignment Scores:
Pred. No.: 1,97e-165 Length: 704
Score: 159.00 Matches: 189
Percent Similarity: 98.95% Conservative: 0
Best Local Similarity: 98.95% Mismatches: 1
Query Match: 62.11% Indels: 2
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-08-956-171E-772 (1-704)

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Db 24 ATGTTAAATCTTGAACAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 83
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeu-GlyAlaLysLeuValPheThrTyrAr 40
Db 84 GCTTTTGGTGTGCGTAAAGCTTTTAGATCAATT-MGGTGTCTAAATTTAGTATTACTTACCG 142
QY 40 GlySGLuArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAl 60
Db 143 TAAAGAACGTAGCCGTAAGAGCTTGAAAAATTTATTAGAACAAATTTAAATCAACCAAGAGC 202
QY 60 aHisLeuTyrGlnIleAspValGlnSerAspGluValIleMetGlyValAlaAsnLysArgSerIle 20
Db 24 ATGTTAAATCTTGAACAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 83
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeu-GlyAlaLysLeuValPheThrTyrAr 40
Db 84 GCTTTTGGTGTGCGTAAAGCTTTTAGATCAATT-MGGTGTCTAAATTTAGTATTACTTACCG 142
QY 40 GlySGLuArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAl 60
Db 143 TAAAGAACGTAGCCGTAAGAGCTTGAAAAATTTATTAGAACAAATTTAAATCAACCAAGAGC 202
QY 60 aHisLeuTyrGlnIleAspValGlnSerAspGluValIleMetGlyValAlaAsnLysArgSerIle 80
Db 203 GCACCTTATCAATTTGATGTTCAAAGCGATGAAGAGGTTTAAATGCTTTTGACCAAT 262
QY 80 eGlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGl 100
Db 263 TGGTAAAGATGTTGGCAATATTGATGGTGATATCATTCATCAATCGCATTTGCTAATATGGA 322
QY 100 uAspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIl 120
Db 323 AGACTTACGCGACGCTTTTCTGAAACTTCACGTGAAGGCTTCTTTGTAGCTCAAGACAT 382
QY 120 eSerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGl 140
Db 383 TAGTCTTACTATTAAACAAATTTGGCTCATGAAGCTTAAAAATTTAATGCCAAGAGTGG 442
QY 140 ySerIleValAlaThrThrTyrLeuGlyGlyPheAlaValGlnAsnTyrAsnValMe 160
Db 443 TAGCATTGTTGCAACACATATTAGTGGCGAAATTCGCAGTTCAAAACTATAATGTGAT 502
QY 160 tGlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPr 180
Db 503 GGGTGTGCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTATTAGCATTTAGACTTAGGTCC 562
QY 180 oAspAsnIleArgValAsnAlaIleSerAla 190

RESULT 5
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; Sequence 772, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
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;
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 772:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 704 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-772

Alignment Scores:
Pred. No.: 1,97e-165 Length: 704
Score: 159.00 Matches: 189
Percent Similarity: 98.95% Conservative: 0
Best Local Similarity: 98.95% Mismatches: 1
Query Match: 62.11% Indels: 2
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-08-781-986A-772 (1-704)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyValAlaAsnLysArgSerIle 20
Db 24 ATGTTAAATCTTGAACAACAAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 83
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeu-GlyAlaLysLeuValPheThrTyrAr 40
Db 84 GCTTTTGGTGTGCGTAAAGCTTTTAGATCAATT-MGGTGTCTAAATTTAGTATTACTTACCG 142
QY 40 GlySGLuArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAl 60
Db 143 TAAAGAACGTAGCCGTAAGAGCTTGAAAAATTTATTAGAACAAATTTAAATCAACCAAGAGC 202
QY 60 aHisLeuTyrGlnIleAspValGlnSerAspGluValIleMetGlyValAlaAsnLysArgSerIle 80
Db 203 GCACCTTATCAATTTGATGTTCAAAGCGATGAAGAGGTTTAAATGCTTTTGACCAAT 262
QY 80 eGlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGl 100
Db 263 TGGTAAAGATGTTGGCAATATTGATGGTGATATCATTCATCAATCGCATTTGCTAATATGGA 322
QY 100 uAspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIl 120
Db 323 AGACTTACGCGACGCTTTTCTGAAACTTCACGTGAAGGCTTCTTTGTAGCTCAAGACAT 382
QY 120 eSerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGl 140
Db 383 TAGTCTTACTATTAAACAAATTTGGCTCATGAAGCTTAAAAATTTAATGCCAAGAGTGG 442
QY 140 ySerIleValAlaThrThrTyrLeuGlyGlyPheAlaValGlnAsnTyrAsnValMe 160
Db 443 TAGCATTGTTGCAACACATATTAGTGGCGAAATTCGCAGTTCAAAACTATAATGTGAT 502
QY 160 tGlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPr 180
Db 503 GGGTGTGCTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTATTAGCATTTAGACTTAGGTCC 562
QY 180 oAspAsnIleArgValAsnAlaIleSerAla 190
```

DB 563 AGATAATATTCGGTTAATGCAATTTCAGCT 593
|||||

RESULT 6

US-08-956-171E-514/c

; Sequence 514, Application US/08956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; Gil H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barash

; Michael R. Fannon

; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

; NUMBER OF SEQUENCES: 5256

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/956,171E

; FILING DATE: 20-Oct-1997

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009,861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781,986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46,789

; REFERENCE/DOCKET NUMBER: PB248P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 514:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 587 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 514:

US-08-956-171E-514

Alignment Scores:

Pred. No.: 8.16e-27 Length: 587

Score: 33.00 Matches: 33

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 12.89% Indels: 0

DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-08-956-171E-514 (1-587)

QY 224 ValGluValGlyThrAlaAlaTyrLeuLeuSerAspLeuSerSerGlyValThrGly 243

DB 586 GTAGAAGTAGGTAAACCTCGGCTTACTTATTAAAGTATTATCAAGTGGCGTTACAGCT 527

QY 244 GluAenIleHisValAspSerGlyPheHisAlaIleLys 256

DB 526 GAAATATTTCATGTAGTAGCGGATTCACGCAATTAAA 488

RESULT 7

US-08-781-986A-514/c

; Sequence 514, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MSDOS version 6.2

; SOFTWARE: ASCII Text

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/781,986A

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Benson, Bob

; REGISTRATION NUMBER: 30,446

; REFERENCE/DOCKET NUMBER: PB248PP

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (301) 309-8504

; TELEFAX: (301) 309-8512

; INFORMATION FOR SEQ ID NO: 514:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 587 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-781-986A-514

Alignment Scores:

Pred. No.: 8.16e-27 Length: 587

Score: 33.00 Matches: 33

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 12.89% Indels: 0

DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-08-781-986A-514 (1-587)

QY 224 ValGluValGlyThrAlaAlaTyrLeuLeuSerAspLeuSerSerGlyValThrGly 243

DB 586 GTAGAAGTAGGTAAACCTCGGCTTACTTATTAAAGTATTATCAAGTGGCGTTACAGCT 527

QY 244 GluAenIleHisValAspSerGlyPheHisAlaIleLys 256

DB 526 GAAATATTTCATGTAGTAGCGGATTCACGCAATTAAA 488

RESULT 8

US-09-134-001C-1172

; Sequence 1172, Application US/09134001C

; Patent No. 6380370

; GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS

; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: GTC-007

; CURRENT APPLICATION NUMBER: US/09/134,001C

; CURRENT FILING DATE: 1998-08-13

; PRIOR APPLICATION NUMBER: US 60/064,964

; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14

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; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 1172
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-1172

Alignment Scores:
Pred. No.: 1.38e-25 Length: 783
Score: 32.00 Matches: 59
Percent Similarity: 96.72% Conservative: 0
Best Local Similarity: 96.72% Mismatches: 1
Query Match: 12.50% Indels: 2
DB: 3 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-134-001C-1172 (1-783)

QY 153 AlaValGlnAsnTyrAsnValMetGlyValAlaLysAlaSerLeuGluAlaAsnValLys 172
DB 469 GCAGTTCAAAATAATATGTTATGGGTAGCTAAGCAAGTTTAGAGCGGATGTTAAA 528

QY 173 TyrLeuAlaLeuAspLeuGlyPro-AspAsnIleArgValAsnAlaIleSerAlaGlyPr 192
DB 529 TATTTAGCTTTAGACTTAGGTGA-AGATAAATATTCGTGTCRAATGCTATTTCTGCAGGGCC 587

QY 192 oileArgThrIeuSerAlaLysGlyValGlyGlyPheAsnThrIleLeuLysGluIleGl 212
DB 588 AATTCGTACTTTAAGTGCTAAAGGTAGGTGGATTAAATACAATTTCTTAAAGAAATTGA 647

QY 212 u 212
DB 648 A 648

RESULT 9
US-09-540-236-500
; Sequence 500, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 500
; LENGTH: 906
; TYPE: DNA
; ORGANISM: M. catarrhalis
US-09-540-236-500

Alignment Scores:
Pred. No.: 1.04e-05 Length: 906
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.47% Indels: 0
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-540-236-500 (1-906)

QY 193 IleArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196
DB 640 ATTGCTGTCATAGCCATCAGTCAGGCGCCCTATTCGACGCTG 681

RESULT 10
US-09-328-352-4085
; Sequence 4085, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 2000-06-16
; PRIOR FILING DATE: 1999-06-16
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4085
; LENGTH: 912
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4085

Alignment Scores:
Pred. No.: 1.05e-05 Length: 912
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.47% Indels: 0
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-328-352-4085 (1-912)

QY 193 IleArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196
DB 661 ATCCGTGTAACGCAATTTCTGCTGTCCTCAATTCGTAATTGTA 702

RESULT 11
US-09-596-002-31
; Sequence 31, Application US/09596002
; Patent No. 6632636
; GENERAL INFORMATION:
; APPLICANT: Lagace, Robert, E.
; APPLICANT: Patterson, Chandra
; APPLICANT: Berg, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: PM-0008-4 US
; CURRENT APPLICATION NUMBER: US/09/596,002
; CURRENT FILING DATE: 2000-06-16
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PERL Program
; SEQ ID NO 31
; LENGTH: 65792
; TYPE: DNA
; ORGANISM: M. catarrhalis
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte template ID No. 6632636 31
; PUBLICATION INFORMATION:
US-09-596-002-31

Alignment Scores:
Pred. No.: 0.000799 Length: 65792
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.47% Indels: 0
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-596-002-31 (1-65792)

QY 183 IleArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196
DB 32004 ATTGCTGTCATAGCCATCAGTCAGGCGCCCTATTCGACGCTG 32045

RESULT 12
US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
; APPLICANT: Fleischmann et al.
; TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
```


;/ NUMBER OF SEQUENCES: 1
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Human Genome Sciences, Inc.
;/ STREET: 9410 Key West Avenue
;/ CITY: Rockville
;/ STATE: MD
;/ COUNTRY: USA
;/ ZIP: 20850
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: 3 1/2 inch diskette
;/ COMPUTER: Dell Pentium
;/ OPERATING SYSTEM: MS DOS v6.22
;/ SOFTWARE: ASCII Text
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/557,884
;/ FILING DATE: 25-Apr-2000
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/476,102
;/ FILING DATE: JUN-5-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Michelle S. Marks
;/ REGISTRATION NUMBER: 41,971
;/ REFERENCE/DOCKET NUMBER: PB186P3
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 301-309-8504
;/ TELEFAX: 301-309-8439
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 1830121 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: double
;/ TOPOLOGY: linear
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-557-884-1

Alignment Scores:
Pred. No.: 0.0232 Length: 1830121
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.47% Indels: 0
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-557-884-1 (1-1830121)

Qy 183 ileArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196
Db 1810914 ATTCGTGTGAATGCAATCTCTGCAGGCCCAATCCGACCCTA 1810873

RESULT 13
US-09-643-990A-1/c
; Sequence 1, Application US/09643990A
; Patent No. 6528289
; GENERAL INFORMATION:
; APPLICANT: Robert D. Fleischmann
; Mark D. Adams
; Owen White
; Hamilton O. Smith
; J. Craig Venter
; TITLE OF INVENTION: The Nucleotide sequence of
; the Haemophilus influenzae Rd Genome, Fragments
; Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette

;/ COMPUTER: Dell Pentium
;/ OPERATING SYSTEM: MS DOS v6.22
;/ SOFTWARE: ASCII Text
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/643,990A
;/ FILING DATE: 23-Aug-2000
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/487,429
;/ FILING DATE: 1995-06-07
;/ APPLICATION NUMBER: 08/426,787
;/ FILING DATE: 1995-04-21
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Kenley K. Hoover
;/ REGISTRATION NUMBER: 40,302
;/ REFERENCE/DOCKET NUMBER: PB186PIC1
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 301-610-5790
;/ TELEFAX: 310-309-8439
;/ INFORMATION FOR SEQ ID NO: 1:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 1830121 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: double
;/ TOPOLOGY: linear
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-643-990A-1

Alignment Scores:
Pred. No.: 0.0232 Length: 1830121
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.47% Indels: 0
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-643-990A-1 (1-1830121)

Qy 183 ileArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196
Db 1810914 ATTCGTGTGAATGCAATCTCTGCAGGCCCAATCCGACCCTA 1810873

RESULT 14
US-09-489-039A-768
; Sequence 768, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 768
; LENGTH: 813
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-768

Alignment Scores:
Pred. No.: 0.000118 Length: 813
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.08% Indels: 0
DB: 4 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-489-039A-768 (1-813)

Qy 184 ArgValAsnAlaIleSerAlaGlyProIleArgThrLeu 196

```
Db          571 CGCGTCAATGCCATCTCTGCCGCTCTATCCGTACGCTG 609
|||||
RESULT 15
US-10-089-740-1
; Sequence 1, Application US/10089740
; Patent No. 6730684
; GENERAL INFORMATION:
; APPLICANT: Miller, William H.
; APPLICANT: Newlander, Kenneth A.
; APPLICANT: Seefeld, Mark A.
; APPLICANT: Uzinskas, Irene N.
; TITLE OF INVENTION: Fab I Inhibitors
; FILE REFERENCE: P51038
; CURRENT APPLICATION NUMBER: US/10/089,740
; CURRENT FILING DATE: 2000-10-10
; PRIOR APPLICATION NUMBER: 60/158,707
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-089-740-1

Alignment Scores:
Pred. No.:      0.0109      Length:      39
Score:          10.00      Matches:     10
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      3.91%      Indels:     0
DB:               4      Gaps:         0

US-08-790-043B-2 (1-256) x US-10-089-740-1 (1-39)

QY          1 MetLeuAsnLeuGluAsnLysThrTyrVal 10
|||||
Db          10 AUGTTAAATCTTGAAGAAACAAACATATATGTC 39
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Search completed: September 6, 2005, 14:41:06
Job time : 704 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 6, 2005, 13:10:24 ; Search time 617 Seconds
(without alignments)
2717.215 Million cell updates/sec

Title: US-08-790-043B-2
Perfect score: 256
Sequence: 1 MLNLENTVYIMGIAKRSI.....LSSGVGTGNIHVDGFGHAIK 256

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 738684 seqs, 3274456166 residues

Word size: 1

Total number of hits satisfying chosen parameters: 14665415

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=Published Applications NA -QFNT=fasap -SUFFIX=rnnpb -MINMATCH=0.1
-LOOPCU=0 -LOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo
-TRANS=human40.ccl -LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=15 -MODE=local -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US08790043 @CIGN 1 723 @runat_06092005_101257_4976
-NCPU=6 -ICPU=3 -MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

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- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq*
- 13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq*
- 14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq*
- 15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq*
- 16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq*
- 17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq*
- 18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq*
- 19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq*
- 20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq*
- 21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq*
- 22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq*
- 23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq*
- 24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq*
- 25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq*
- 26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	256	100.0	768	9	US-09-815-242-4173	Sequence 4173, Ap
2	256	100.0	771	9	US-09-815-242-8437	Sequence 8437, Ap
3	256	100.0	771	9	US-09-815-242-8794	Sequence 8794, Ap
4	256	100.0	771	17	US-10-282-122A-7734	Sequence 7734, Ap
5	256	100.0	771	21	US-10-857-625-263	Sequence 263, Ap
6	256	100.0	771	21	US-10-888-524-1	Sequence 1, Appl
7	256	100.0	6985	21	US-10-857-625-34	Sequence 34, Appl
8	190	74.2	916	16	US-10-138-701-5	Sequence 5, Appl
9	190	74.2	916	20	US-10-823-785-5	Sequence 5, Appl
10	159	62.1	704	8	US-08-781-986A-772	Sequence 772, App
11	159	62.1	704	18	US-10-329-624-772	Sequence 772, App
c 12	152	59.4	552	9	US-09-815-242-1952	Sequence 1952, Ap
c 13	152	59.4	552	9	US-09-815-242-1963	Sequence 1963, Ap
c 14	152	59.4	552	17	US-10-282-122A-4490	Sequence 4490, Ap
c 15	152	59.4	552	17	US-10-282-122A-4491	Sequence 4491, Ap
c 16	107	41.8	324	9	US-09-815-242-1697	Sequence 1697, Ap
c 17	107	41.8	324	9	US-09-815-242-3050	Sequence 3050, Ap
c 18	107	41.8	324	17	US-10-282-122A-4224	Sequence 4224, Ap
c 19	107	41.8	324	17	US-10-282-122A-5569	Sequence 5569, Ap
c 20	96	37.5	289	9	US-09-815-242-1666	Sequence 1666, Ap
c 21	96	37.5	289	17	US-10-282-122A-4233	Sequence 4233, Ap
c 22	73	28.5	229	9	US-09-815-242-2214	Sequence 2214, Ap
c 23	73	28.5	229	9	US-09-815-242-2218	Sequence 2218, Ap
c 24	73	28.5	229	9	US-09-815-242-2219	Sequence 2219, Ap
c 25	73	28.5	229	9	US-09-815-242-2529	Sequence 2529, Ap
c 26	73	28.5	229	9	US-09-815-242-3421	Sequence 3421, Ap
c 27	73	28.5	229	17	US-10-282-122A-4728	Sequence 4728, Ap
c 28	73	28.5	229	17	US-10-282-122A-4739	Sequence 4739, Ap
c 29	73	28.5	229	17	US-10-282-122A-4747	Sequence 4747, Ap
c 30	73	28.5	229	17	US-10-282-122A-5075	Sequence 5075, Ap
c 31	73	28.5	229	17	US-10-282-122A-5976	Sequence 5976, Ap
c 32	41	16.0	363	17	US-10-282-122A-35143	Sequence 35143, A
c 33	33	12.9	101	9	US-09-815-242-3021	Sequence 3021, Ap
c 34	33	12.9	101	17	US-10-282-122A-5575	Sequence 5575, Ap
c 35	33	12.9	587	8	US-08-781-986A-514	Sequence 514, App
c 36	33	12.9	587	18	US-10-329-624-514	Sequence 514, App
c 37	32	12.5	768	17	US-10-282-122A-34355	Sequence 34355, A
c 38	32	12.5	768	22	US-10-724-972A-2044	Sequence 2044, Ap
c 39	20	7.8	768	17	US-10-282-122A-10473	Sequence 10473, A
c 40	20	7.8	777	17	US-10-369-493-40175	Sequence 40175, A
c 41	19	7.4	102	9	US-09-815-242-2921	Sequence 2921, Ap
c 42	19	7.4	102	17	US-10-282-122A-5478	Sequence 5478, Ap
c 43	15	5.9	780	17	US-10-369-493-43741	Sequence 43741, A
c 44	15	5.9	783	17	US-10-369-493-41051	Sequence 41051, A
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ALIGNMENTS

RESULT 1

US-09-815-242-4173
; Sequence 4173, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; PROKARYOTES
; FILE REFERENCE: ELITRA.011A

; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4173
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; US-09-815-242-4173

Alignment Scores:
Pred. No.: 1,89e-256 Length: 768
Score: 256.00 Matches: 256
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-815-242-4173 (1-768)

Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
Db 1 ATGTTAAATCTTGAAACAAACAAATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60
Qy 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
Db 61 GCTTTTGGTGCCTAAAGTTTGTAGATCAATTAGGTGCTAAAATTAGTATTTACTTACCGT 120
Qy 41 LysGluArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAla 60
Db 121 AAAGAAGTAGCGGTAAAGCTTGAAAATTTATTAGACAATTAATCAACAGAGCG 180
Qy 61 HisLeuTyrGlnIleAspValGlnSerAspGluValIleAsnGlyPheGluGlnIle 80
Db 181 CACTTATATCAAAATTCATGTTCAAGCGATGAAGAGTTATTAAATGTTTTCAGCAAAAT 240
Qy 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
Db 241 GGTAAAGATGTTGGCAATATCGATGGTGTATATCATTCATCGCAATTCGCTAATATGGA 300
Qy 101 AspLeuArgGlyValArgPheSerGluThrSerArgGluGlyPheLeuAlaGlnAspIle 120
Db 301 GATTTACGGGAGCTTTTCTGAACTTCACGTGAAGGTTTCTGTGATGCCCAAGACATT 360
Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
Db 361 AGTTCTTACTCACTAATCTATCGTTGCTCATGAAGCTAAAAAATTAATGCCAAGAGTGT 420
Qy 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPheAlaValGlnAsnTyrAsnValMet 160
Db 421 AGCATTTGTTGCAACAACATATTTAGTGGCGAATTCGCAGTTTCAAACTTACAAATGTGATG 480
Qy 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
Db 481 GGTGTTGCTTAAGCGAGCTTAGNAGCAATGTAATATTTAGCATTAGCATTAGTCCA 540
Qy 181 AspAsnIleArgValAsnAlaIleSerAlaGlyProIleArgThrIleuSerAlaLysGly 200
Db 541 GATAATATTCGGCTTAATGCAATTTTCAGCTGGTCCAATCCGTACATTAAGTCAAAAGGT 600

Qy 201 ValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgSer 220
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Qy 221 ValAspGlnValGluValGlyLysThrAlaAlaTyrLeuLeuSerAspLeuSerSerGly 240
Db 661 GTTGATCAAGTAGAAGTAGGTAAACACAGCGGCTTACTTATTAAAGTACTTATCAAGTGC 720
Qy 241 ValThrGlyGluAsnIleHisValAspSerGlyPheHisAlaIleLys 256
Db 721 GTTACAGGTGAAATATATTTCATGTAGATAGCGGATTCACGCAATTAATA 768

RESULT 2

US-09-815-242-8437
; Sequence 8437, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8437
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(771)
US-09-815-242-8437

Alignment Scores:
Pred. No.: 1.9e-256 Length: 771
Score: 256.00 Matches: 256
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-815-242-8437 (1-771)

Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
Db 1 ATGTTAAATCTTGAAACAAACAAATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60
Qy 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
Db 61 GCTTTTGGTGCCTAAAGTTTTCAGATCAATTAGGTGCTAAAATTAGTATTTACTTACCGT 120

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Qy 61 HisLeuTyrGlnIleAspValGlnSerAspGluValIleAsnGlyPheGluGlnIle 80
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Db 181 CACTTATCAAAATGATGTTCAAGCGGATGAAGAGTTATTATGTTTTGAGCAAAAT 240
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Qy 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
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Db 241 GGTAAAGATGTTGCAATATCGATGTTGATATCAATTCATCGCAATTTGCTAATATGGA 300
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Qy 101 AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
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Db 301 GATTTACGCGAGCGTTTCTGAAACTTCACGTGAAGGTTTCTTGTGTAGCCCAAGACATT 360
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Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
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Db 421 AGCATTTGTCACACACATATTTAGGTGGCGAATTCGCAGTTTCAAAACTACAAATGTGATG 480
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Qy 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
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Db 481 GGTGTTGCTAAGCGAGCTTAGAACCAATGTTAAATATTTAGCAATTTAGCTTCA 540
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Qy 201 ValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAsn 220
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Qy 221 ValAspGlnValGluValGlyLysThrAlaAlaTyrIleLeuSerAspLeuSerSerGly 240
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Db 721 GTTACAGGTGAAATAATTATCAATAGATAGCGGATTCACGCAATTA 768
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RESULT 3
US-09-815-242-8794
; Sequence 8794, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
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; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8794
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(771)
US-09-815-242-8794
Alignment Scores:
Pred. No.: 1,9e-256 Length: 771
Score: 256.00 Matches: 256
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0
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Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
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Db 1 ATGTTAAATCTTTGAAACCAACATATGTCATCATCGGAATCGCTAATAAGCGTAGTATT 60
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Qy 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
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|
Db 61 GCTTTTGGTGTGCTAAAGTTTTAGATCAATTAGGTGCTAAATTAGTATTATTACTTACCGT 120
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|
Qy 41 LysGluArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAla 60
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|
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Db 121 AAAGAACGTAGCGGTAAAGAGCTTGAAATAATTTATAGACAAATTAATCAACCAAGAGCG 180
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|
|
Qy 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
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Db 181 CACTTATATCAAAATGATGTTCAAGCGCATGAAGAGGTTATTAAATGGTTTTCAGCAAAAT 240
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|
Qy 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
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Db 241 GGTAAAGATGTTGGCAATATTTGATGTTATATCATTCATTCATCGCAATTCCTAATATGGA 300
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|
Qy 101 AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
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Db 301 GACTTACGCGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
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Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
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Db 361 AGTTCTTACTCATTAACCAATTTGGTCTCATGAAGCTTAAATAATTAATGCCAAGAGTGGT 420
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Qy 141 SerIleValAlaThrTyrLeuGlyGlyGluPheAlaValGlnAsnTyrAsnValMet 160
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Db 421 AGCATTTGTCACACACATATTTAGGTGGCGAATTCGCAGTTTCAAAACTATTAATGTGATG 480
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Qy 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
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Db 481 GGTGTTGCTAAGCGAGCTTAGAACCAATGTTAAATATTTAGCATTAGCTTACGTGCCA 540
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Qy 181 AspAsnIleArgValAsnAlaIleSerAlaGlyProIleArgThrIleuSerAlaLysGly 200
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Qy 201 ValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAsn 220
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Db 601 GTGGTGTGTTTCAATCAATTTCTTAAGAAATCGAAGAGCGTGCACCTTTAAACGTAA 660
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Qy 221 ValAspGlnValGluValGlyLysThrAlaAlaTyrLeuSerAspLeuSerSerGly 240
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QY 241 ValThrGlyGluAsnIleHisValAspSerGlyPheHisAlaIleLys 256
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Db 721 GTTACAGGTGAATAATTCTCATGTAGATAGCGGATTCACGCAATTAAA 768

RESULT 4

US-10-282-122A-7734
; Sequence 7734, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7734
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

US-10-282-122A-7734

Alignment Scores:
Pred. No.: 1,9e-256 Length: 771
Score: 256.00 Matches: 256
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 17 Gaps: 0

US-08-790-043B-2 (1-256) x US-10-282-122A-7734 (1-771)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
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Db 1 ATGTTAAATCTTGAAACAAAACATATGTCATCGGGAATCGCTAATAAGCGTAGTATT 60
|
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
|
Db 61 GCTTTGGTGCCTAAAGTTTTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 120
|
QY 41 LysGluArgSerArgLysGluLeuGluLysLeuLeuGluLysLeuLeuAsnGlnProGluAla 60
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Db 121 AAAGAACGTAGCCGTAAAGAGCTTGAAATAATTATTAGAACAAATTAATAATCAACCAAGCG 180
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QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
|
Db 181 CACTTATATCAAAATGATGTTCAAAGCGATGAAGAGGTATTAAATGTTGTTTGGAGCAAAAT 240
|
QY 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
|
Db 241 GGTAAAGATGTTGGCAATATTGATGGTGTATATCATTCATTCGCAATTTGCTAATAATGAA 300
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QY 101 AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
|
Db 301 GACTTACGGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTTAGCTCAAGACATT 360
|
QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
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Db 361 AGTTCTTACTCATTAACAATTTGTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGTGGT 420
|
QY 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPheAlaValGlnAsnTyrAsnValMet 160
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Db 421 AGCATGTTGCAACAACATATTTAGTGGCGAATTCGCAGTTCAAAATTTAATATGTGATG 480
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QY 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
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Db 481 GGTGTTGCTAAAGCGAGCTTAGAAGCAATGTTAAATATTATTAGCATTTAGCTTAGTCTCT 540
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QY 181 AspaenIleArgValAsnAlaIleSerAlaGlyProIleArgThrLeuSerAlaLysGly 200
|
Db 541 GATATATTCGGTTAAATGCAATTTTCAGTGGTCCAATCCGTTACATTAAAGTGCAAAAGGT 600
|
QY 201 ValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAsn 220
|
Db 601 GTGGTGGTTTCAATACAAATTTTAAAGAAATCGAAGAGCGTGACCTTTAAACGTAAC 660
|
QY 221 ValAspGlnValGluValGlyThrAlaAlaTyrLeuLeuSerAspLeuSerSerGly 240
|
Db 661 GTTGATCAAGTAGAAGTAGGTAAACACGCGCTTACTTTATTAAAGTGACTTTATCAAGTGGC 720
|
QY 241 ValThrGlyGluAsnIleHisValAspSerGlyPheHisAlaIleLys 256
|
Db 721 GTTACAGGTGAATAATTATTCTATGTAGATAGCGGATTCACGCAATTAAA 768
|

RESULT 5

US-10-857-625-263

; Sequence 263, Application US/10857625
; Publication No. US20050026189A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: MICROBIAL OPERONS
; FILE REFERENCE: ELITRA.036A
; CURRENT APPLICATION NUMBER: US/10/857,625
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 60/474768
; PRIOR FILING DATE: 2003-05-29
; NUMBER OF SEQ ID NOS: 833
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 263
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

US-10-857-625-263

Alignment Scores:
Pred. No.: 1,9e-256 Length: 771
Score: 256.00 Matches: 256
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-08-790-043B-2 (1-256) x US-10-857-625-263 (1-771)

QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
DB 1 ATGTTAAATCTTGAACCAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyValAlaLysLeuValPheThrTyrArg 40
DB 61 GCTTTTGGTGTCCGTAAGTTTGTAGATCAATAGGTGCTAATATTAGTATTACTTACCGT 120
QY 41 LysGluArgSerArgLysGluLeuGlyLysLeuLeuGluAsnGlnProGluAla 60
DB 121 AAAGAACGTAGCGTAAAGAGCTTGAATAATATTAGAACATTAATCAACCCAGAAGCG 180
QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluValIleAsnGlyPheGluGlnIle 80
DB 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGGTATTAAATGTTTGTAGCAAAAT 240
QY 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
DB 241 GGTAAAGATGTTGGCAATATTGATGGTGTATATCAATCGCATTTGCTAATATGGAA 300
QY 101 AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
DB 301 GACTTACGCGGACGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
DB 361 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAGAAATTAATGCCAGAAGTGGT 420
QY 141 SerIleValAlaThrTyrLeuGlyGlyPheAlaValGlnAsnTyrAsnValMet 160
DB 421 AGCATTTGTCACACACATATTAGGTGGCAATTCGAGTTCAAATAATTATATATGTGATG 480
QY 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
DB 481 GGTGTTGCTAAAGGAGCTTAGAAGCAATGTTAATATTATAGCATTAGCTTAGCTCT 540
QY 181 AspAsnIleArgValAsnAlaIleSerAlaGlyProIleArgThrLeuSerAlaLysGly 200
DB 541 GATAATATTCCGCTTAATGCAATTTCCAGTGGTCCCAATCCGTACATTAAGTGCNAAAGT 600
QY 201 ValGlyGlyPheAsnThrIleLeuLysGluIleGluArgAlaProLeuLysArgAsn 220
DB 601 GTGGGTGGTTTCAATCAATTTCTTAAGAAATCGAAGAGCGTGCACCTTTAAACGTAAC 660
QY 221 ValThrGlyLysLeuHisValAspSerGlyPheHisAlaIleLys 256
DB 721 GTTACAGGTGAAATATTTCATGTAGATAGCGGATTCACGCAATTAA 768

RESULT 6

US-10-888-524-1
; Sequence 1, Application US/10888524
; Publication No. US20050112713A1
; GENERAL INFORMATION:
; APPLICANT: DEWOLF JR., WALTER E.
; APPLICANT: PAYNE, DAVID JOHN
; APPLICANT: MILNER, PETER HENRY
; APPLICANT: PEARSON, STEWART CAMPBELL
; APPLICANT: LONSDALE, JOHN TIMOTHY
; TITLE OF INVENTION: METHODS OF USING FAB I AND COMPOUNDS MODULATING FAB I ACTIVITY
; FILE REFERENCE: IPT-061.02
; CURRENT APPLICATION NUMBER: US/10/888,524
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: 60/024,845
; PRIOR FILING DATE: 1996-08-28
; PRIOR APPLICATION NUMBER: 08/790,043
; PRIOR FILING DATE: 1997-08-28
; PRIOR APPLICATION NUMBER: 60/134,362
; PRIOR FILING DATE: 1999-05-14

; PRIOR APPLICATION NUMBER: 10/009,219
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: PCT/US00/12104
; PRIOR FILING DATE: 2000-05-04
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 1
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-888-524-1
Alignment Scores:
Pred. No.: 1,9e-256 Length: 771
Score: 256.00 Matches: 256
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0
US-08-790-043B-2 (1-256) x US-10-888-524-1 (1-771)
QY 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
DB 1 ATGTTAAATCTTGAACCAACATATGTCATCGGAATCGCTAATAAGCGTAGTATT 60
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyValAlaLysLeuValPheThrTyrArg 40
DB 61 GCTTTTGGTGTCCGTAAGTTTGTAGATCAATAGGTGCTAATATTAGTATTACTTACCGT 120
QY 41 LysGluArgSerArgLysGluLeuGlyLysLeuLeuGluAsnGlnProGluAla 60
DB 121 AAAGAACGTAGCGTAAAGAGCTTGAATAATATTAGAACATTAATCAACCCAGAAGCG 180
QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
DB 181 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGGTATTAAATGTTTGTAGCAAAAT 240
QY 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
DB 241 GGTAAAGATGTTGGCAATATTGATGGTGTATATCAATCGCATTTGCTAATATGGAA 300
QY 101 AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
DB 301 GACTTACGCGGACGCTTTCTGAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 360
QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
DB 361 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAGAAATTAATGCCAGAAGTGGT 420
QY 141 SerIleValAlaThrTyrLeuGlyGlyPheAlaValGlnAsnTyrAsnValMet 160
DB 421 AGCATTTGTCACACACATATTAGGTGGCAATTCGAGTTCAAATAATTATATATGTGATG 480
QY 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
DB 481 GGTGTTGCTAAAGGAGCTTAGAAGCAATGTTAATATTATAGCATTAGCTTAGCTCT 540
QY 181 AspAsnIleArgValAsnAlaIleSerAlaGlyProIleArgThrLeuSerAlaLysGly 200
DB 541 GATAATATTCCGCTTAATGCAATTTCCAGTGGTCCCAATCCGTACATTAAGTGCNAAAGT 600
QY 201 ValGlyGlyPheAsnThrIleLeuLysGluIleGluArgAlaProLeuLysArgAsn 220
DB 601 GTGGGTGGTTTCAATCAATTTCTTAAGAAATCGAAGAGCGTGCACCTTTAAACGTAAC 660
QY 221 ValThrGlyLysLeuHisValAspSerGlyPheHisAlaIleLys 240
DB 661 GTTGTACAGTAGAAGTAGTAAACACGCGGCTTACTTTRTTAAAGTGACCTTATCAAGTGC 720
QY 241 ValThrGlyLysLeuHisValAspSerGlyPheHisAlaIleLys 256
DB 721 GTTACAGGTGAAATATTTCATGTAGATAGCGGATTCACGCAATTAA 768


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Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
Db 456 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGGTGGT 515
Qy 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPheAlaValAlaGlnAsnTyrAsnValMet 160
Db 516 AGCATTTGTCACACACATATTTAGGTGGCAATTCGCAGTTCAAAACTATATATGTGATG 575
Qy 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
Db 576 GGTGTTCTAAAGCGAGCTAGGAAGCAAAATGTTAAATATTTAGCATTAGACTTAGGTCCA 635
Qy 181 AspAsnIleArgValAsnAlaIleSerAlaGly-ProIleArgThrLeuSerAlaLysG1 200
Db 636 GATAAATATTCGCGTTAATGCAATTTCCAGTAG-TCCAATCCGTACATTAAGTGCAAAAGG 694
Qy 200 YValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAs 220
Db 695 TGTGGGTGGTTTCNATACAAATTTTAAAGAAATCGAAGAGCGTGCACCTTTTAAACGTAA 754
Qy 220 nValAspGlnValGluValGlyLysThrAlaAlaTyrLeuLeuSerAspLeuSerSerG1 240
Db 755 TGTGATCAAGTAGAAGTAGTAAACTCGCGCTTACTTATTAAAGTGAATTTATCAAGTGG 814
Qy 240 YValThrGlyGluAsnIleHisValAspSerGlyPheHisAlaIleLys 256
Db 815 CGTTACAGGTGAAATATTCATGTAGATAGCGGATTCCACGCAATTTAAA 863

RESULT 9
US-10-823-785-5
; Sequence 5, Application US/10823785
; Publication No. US20040265962A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc. et al.
; TITLE OF INVENTION: Staphylococcus aureus genes and polypeptides
; FILE REFERENCE: PB484
; CURRENT APPLICATION NUMBER: US/10/823,785
; CURRENT FILING DATE: 2004-04-14
; PRIOR APPLICATION NUMBER: US/09/512,255
; PRIOR FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/098,964
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: US 60/009,861
; PRIOR FILING DATE: 1996-01-05
; PRIOR APPLICATION NUMBER: PCT/ US99/19726
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: US 08/956,171
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 916
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-823-785-5

Alignment Scores:
Pred. No.: 1-23e-187 Length: 916
Score: 190.00 Matches: 255
Percent Similarity: 99.22% Conservative: 0
Best Local Similarity: 99.22% Mismatches: 1
Query Match: 74.22% Indels: 2
DB: 20 Gaps: 0

US-08-790-043B-2 (1-256) x US-10-823-785-5 (1-916)
Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
Db 96 ATGTTAAATCTTGAAACAAACATATGTATCATCGGAATCGTAATAAGCGTAGTATT 155
Qy 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
Db 156 GCTTTTGGTGCCTAAAGTTTATGATCAATAGGTGCTAAATAGTATTACTTACCGGT 215
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Qy 41 LysGluArgSerArgLysGluLeuGluLysLeuLeuGluGlnLeuAsnGlnProGluAla 60
Db 216 AAAGAAGCTAGCCGTAAAGAGCTTGAAAAATATTATTAGAACAAATTAATCAACCAAGCG 275
Qy 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
Db 276 CACTTATATCAAAATTCATGTTCAAGCGATGAAGAGGTTATTAAATGGTTTTAGCAAAAT 335
Qy 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
Db 336 GGTAAAGATGTTGGCAATATTGATGTTATATCATTCATTCATTCGTTTGTATATATGGA 395
Qy 101 AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
Db 396 GACTTACCGGAGCGCTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGTCAAGACATT 455
Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
Db 456 AGTTCTTACTCATTAACAATTTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGGTGGT 515
Qy 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPheAlaValGlnAsnTyrAsnValMet 160
Db 516 AGCATTTGTTGCAACACATATTTAGTGGCGAATTCGCAGTTCAAAACTATATATGTGATG 575
Qy 161 GlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPro 180
Db 576 GGTGTTGTTAAAGCGAGCTTAGAAGCAAAATGTTAAATATTTAGCATTAGACTTAGGTCCA 635
Qy 181 AspAsnIleArgValAsnAlaIleSerAlaGly-ProIleArgThrLeuSerAlaLysG1 200
Db 636 GATAAATATTCGCGTTAATGCAATTTCCAGTAG-TCCAATCCGTACATTAAGTGCAAAAGG 694
Qy 200 YValGlyGlyPheAsnThrIleLeuLysGluIleGluGluArgAlaProLeuLysArgAs 220
Db 695 TGTGGGTGGTTTCAATACAAATTCCTTAAAGAAATCGAAGAGCGTGCACCTTTTAAACGTAA 754
Qy 220 nValAspGlnValGluValGlyLysThrAlaAlaTyrLeuLeuSerAspLeuSerSerG1 240
Db 755 TGTGATCAAGTAGAAGTAGTAAACTCGCGCTTACTTATTAAAGTGAATTTATCAAGTGG 814
Qy 240 YValThrGlyGluAsnIleHisValAspSerGlyPheHisAlaIleLys 256
Db 815 CGTTACAGGTGAAATATTCATGTAGATAGCGGATTCCACGCAATTTAAA 863

RESULT 10
US-08-781-986A-772
; Sequence 772, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
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Db 323 AGACTTACGGCGAGCTTTCTTCTGAAGAACTTCACGCGAAGGCTTCTGTGTAGCTCAAGACAT 382
Qy 120 eSerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyG1 140
Db 383 TAGTCTTACTTACATAAATTTGGCTCATGAAGCTTAAAAAATTAAATGCGAGAGGTGG 442
Qy 140 ySerIleValAlaThrThrTyrLeuGlyGlyGluPheAlaValGlnAsnTyrAsnValMe 160
Db 443 TAGCATTTGTTGCAACAACATATTTAGGTGGCGAATTCGCAGTTCAAAACTATAATGTGAT 502
Qy 160 tGlyValAlaLysAlaSerLeuGluAlaAsnValLysTyrLeuAlaLeuAspLeuGlyPr 180
Db 503 GGGTGTGCTTAAAGCGAGCTTAGAAGCAATGTTAAATATTTAGCATTAGACTTAGGTCC 562
Qy 180 oAspAsnIleArgValAlaAsnAlaIleSerAla 190
Db 563 AGATAATATTCGCGTTAATGCAATTTCACTAGCT 593

RESULT 12

US-09-815-242-1952/c
; Sequence 1952, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 1952
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

US-09-815-242-1952
Alignment Scores:
Pred. No.: 2.9e-148 Length: 552
Score: 152.00 Matches: 152
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.38% Indels: 0
DB: 9 Gaps: 0

US-08-790-043B-2 (1-256) x US-09-815-242-1952 (1-552)

Qy 1 MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle 20
Db 456 ATGTTAAATCTTGAAAACAAAACATATGTCATCGTAATCGTAAATAGCGTAGTATT 397

Qy 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLysLeuValPheThrTyrArg 40
Db 396 GCTTTTGGTGTGCTTAAAGTTTAGATCAATTAGGTGCTAAATTAGTATTACTTACCGT 337
Qy 41 LysGluArgSerArgLysGluLeuGlyLysLeuGluGlnLeuAsnGlnProGluAla 60
Db 336 AAGAACGCTAGCGGTAAAGAGCTTGAATAATTTATTAGAACAATAAATCAACGAGGCG 277
Qy 61 HisLeuTyrGlnIleAspValGlnSerAspGluValIleAsnGlyPheGluGlnIle 80
Db 276 CACTTATATCAATTCATGTTCAACGCGATGAAGAGGTTATTAAATGGTTTGGACAAATT 217
Qy 81 GlyLysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu 100
Db 216 GGTAAAGATGTTGGCAATATTGATGCTATATCATTCATCAATGCAATTTGCTAATATGGA 157
Qy 101 AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
Db 156 GACTTACGGCGAGCTTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 97
Qy 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
Db 96 AGTTCCTTACTTAAACAATTTGGCTCATGAAGCTTAAAAAATAATGCGAGAGGTGGT 37
Qy 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPhe 152
Db 36 AGCATTTGTTGCAACACACATATTTAGGTGGCGAATTC 1

RESULT 13

US-09-815-242-1963/c
; Sequence 1963, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard

; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1963
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Staphylococcus aureus

US-09-815-242-1963
Alignment Scores:
Pred. No.: 2.9e-148 Length: 552
Score: 152.00 Matches: 152
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

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Query Match: 59.38% Indels: 0
DB: 9 Gaps: 0
US-08-790-043B-2 (1-256) x US-09-815-242-1963 (1-552)
QY 1 MetLeuAsnLeuGluAenLysThrTyrValIleMetGlyIleAlaAenLysArgSerile 20
DB 456 ATGTTAAATCTTGAAACAACAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 397
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
DB 396 GCTTTTGGTGGCTAAAGCTTTAGATCAATTAGGTGCTAAATTTAGTATTACTTTACCGT 337
QY 41 LysGluArgSerArgLysGluLeuGlyLysLeuLeuGluGlnLeuAsnGlnProGluAla 60
DB 336 AAAGAACGTAGCGGTAAAGAGCTTGAAATAATTTATAGAACAAATTAATCAACCAAGGCG 277
QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
DB 276 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGGTATTAAATGGTTTGGAGCAAT 217
QY 81 GlyLysAspValGlyAenLysLeuAspGlyValTyrHisSerileAlaPheAlaAenMetGlu 100
DB 216 GGTAAAGATGTTGGCAATATTGATGTTATATCAATCGCATTTGCTAATAATGGAA 157
QY 101 AspLeuArgLysArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
DB 156 GACTTACGCGGACGCTTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 97
QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
DB 96 AGTTCTTACTCATTAACAAATTTGGCTCATGAAGCTAAAAAATTAATGCGAAGGTGGT 37
QY 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPhe 152
DB 36 AGCATTTGTTGCAACACATATTTAGTGGCGAATTC 1
RESULT 14
US-10-282-122A-4490/c
; Sequence 4490, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA 034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
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; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4490
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Staphylococcus aureus
US-10-282-122A-4490
Alignment Scores:
Pred. No.: 2.9e-148 Length: 552
Score: 152.00 Matches: 152
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 59.38% Indels: 0
DB: 17 Gaps: 0
US-08-790-043B-2 (1-256) x US-10-282-122A-4490 (1-552)
QY 1 MetLeuAsnLeuGluAenLysThrTyrValIleMetGlyIleAlaAenLysArgSerile 20
DB 456 ATGTTAAATCTTGAAACAACAACATATGTCATCATGGGAATCGCTAATAAGCGTAGTATT 397
QY 21 AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg 40
DB 396 GCTTTTGGTGGCTAAAGCTTTAGATCAATTAGGTGCTAAATTTAGTATTACTTTACCGT 337
QY 41 LysGluArgSerArgLysGluLeuGlyLysLeuLeuGluGlnLeuAsnGlnProGluAla 60
DB 336 AAAGAACGTAGCGGTAAAGAGCTTGAAATAATTTATAGAACAAATTAATCAACCAAGGCG 277
QY 61 HisLeuTyrGlnIleAspValGlnSerAspGluGluValIleAsnGlyPheGluGlnIle 80
DB 276 CACTTATATCAAAATGATGTTCAAGCGATGAAGAGGTATTAAATGGTTTGGAGCAAT 217
QY 81 GlyLysAspValGlyAenLysLeuAspGlyValTyrHisSerileAlaPheAlaAenMetGlu 100
DB 216 GGTAAAGATGTTGGCAATATTGATGTTATATCAATCGCATTTGCTAATAATGGAA 157
QY 101 AspLeuArgLysArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle 120
DB 156 GACTTACGCGGACGCTTTTCTGAAACTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT 97
QY 121 SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly 140
DB 96 AGTTCTTACTCATTAACAAATTTGGCTCATGAAGCTAAAAAATTAATGCGAAGGTGGT 37
QY 141 SerIleValAlaThrThrTyrLeuGlyGlyGluPhe 152
DB 36 AGCATTTGTTGCAACACATATTTAGTGGCGAATTC 1
RESULT 15
US-10-282-122A-4491/c
; Sequence 4491, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
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; APPLICANT: Carr, Grant
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; APPLICANT: Xu, H.
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! TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
! FILE REFERENCE: ELITRA.034A
! CURRENT APPLICATION NUMBER: US/10/282.122A
! CURRENT FILING DATE: 2003-02-20
! PRIOR APPLICATION NUMBER: 60/191,078
! PRIOR FILING DATE: 2000-03-21
! PRIOR APPLICATION NUMBER: 60/206,848
! PRIOR FILING DATE: 2000-05-23
! PRIOR APPLICATION NUMBER: 60/207,727
! PRIOR FILING DATE: 2000-05-26
! PRIOR APPLICATION NUMBER: 60/230,335
! PRIOR FILING DATE: 2000-09-06
! PRIOR APPLICATION NUMBER: 60/230,347
! PRIOR FILING DATE: 2000-09-09
! PRIOR APPLICATION NUMBER: 60/242,578
! PRIOR FILING DATE: 2000-10-23
! PRIOR APPLICATION NUMBER: 60/253,625
! PRIOR FILING DATE: 2000-11-27
! PRIOR APPLICATION NUMBER: 60/257,931
! PRIOR FILING DATE: 2000-12-22
! PRIOR APPLICATION NUMBER: 60/267,636
! PRIOR FILING DATE: 2001-02-09
! PRIOR APPLICATION NUMBER: 60/269,308
! PRIOR FILING DATE: 2001-02-16
! Remaining Prior Application data removed - See File Wrapper or PALM.
! NUMBER OF SEQ ID NOS: 78614
! SOFTWARE: PatentIn version 3.1
! SEQ ID NO 4491
! LENGTH: 552
! TYPE: DNA
! ORGANISM: Staphylococcus aureus
! US-10-282-122A-4491

Alignment Scores:

Pred. No.:	2.9e-148	Length:	552
Score:	152.00	Matches:	152
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	59.38%	Indels:	0
DB:	17	Gaps:	0

US-08-790-043B-2 (1-256) x US-10-282-122A-4491 (1-552)

Qy	1	MetLeuAsnLeuGluAsnLysThrTyrValIleMetGlyIleAlaAsnLysArgSerIle	20
Db	456	ATGTTAAATCTGAAAAACAAACATATGTCATCATGGCAATCGCTAATAAGCGTAGTATT	397
Qy	21	AlaPheGlyValAlaLysValLeuAspGlnLeuGlyAlaLysLeuValPheThrTyrArg	40
Db	396	GCYTTTGGTGTGCGTAAAGTTTGTAGATCAATTAGGTGCTAAATTAGTATTCTTACCTACCGT	337
Qy	41	LysGluArgSerArgLysGluLeuGluLysLeuGluGlnLeuAsnGlnProGluAla	60
Db	336	AAAGAAGTACCGCTAAGAGCTTGAAAATTTATTAGAACATTAATCAACCCAGAGCG	277
Qy	61	HisLeuTyrGlnIleAspValGlnSerAspGluValIleAsnGlyPheGluGlnIle	80
Db	276	CACCTATATCAATTGATGTTCAAAGCGATGAAGAGGTATTAAATGGTTTGGACAAATT	217
Qy	81	GlyIysAspValGlyAsnIleAspGlyValTyrHisSerIleAlaPheAlaAsnMetGlu	100
Db	216	GGTAAAGATGTGGCAATATTGTGGTGTATATCATTCATTCGTCATTTCGCTAATATGGAA	157
Qy	101	AspLeuArgGlyArgPheSerGluThrSerArgGluGlyPheLeuLeuAlaGlnAspIle	120
Db	156	GACTTACCGGACGCTTTTCTGAACCTTCACGTGAAGGCTTCTTGTAGCTCAAGACATT	97
Qy	121	SerSerTyrSerLeuThrIleValAlaHisGluAlaLysLysLeuMetProGluGlyGly	140
Db	96	AGTCTTTACTTCATTAAACAATTGTGGCTCATGAAGCTAAAAAATTAATGCCAGAAGGTG	37
Qy	141	SerIleValAlaThrThrTyrLeuGlyGlyGluPhe	152

Db 36 AGCATTGTTGCCAACACATATTTAGTGGCGAATTC 1

Search completed: September 6, 2005, 16:18:17

Job time : 624 secs

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